

found among the different groups of single-crosses for the rest of the morphological traits studied. The ANOVA shows highly significant differences among single-crosses for all the parametric variables measured (Table 2).

Table 2. ANOVA results (mid-squares) for the morphological traits considered in single-crosses evaluated during 2007/08 in Castelar.

Variation source	PH	EIH	SD	NL	NLUE	EP
Hybrid	708.2**	469.9**	0.18**	3.19**	1.21**	0.13**
Replicate	2.16 ns	9.88 ns	0.0006 ns	0.04 ns	0.0001 ns	0.0001 ns

Tables 3, 4 and 5 summarize all of the information collected in relation to the qualitative traits considered in each single-cross. 59.3% of the single-crosses evaluated have their leaves arranged in normal position in relation to the stems, similar to the dent tester ACA 2000. 77.8% of the materials showed abundant sheath pubescence, and in 52.9% of the single-crosses abundant leaf pubescence was observed.

Table 3. Qualitative traits evaluated in HQP single-crosses during 2007/08.

Hybrid	LC	LP	SP	LPU	LEC
3146	dark green	semierect	abundant	abundant	weak
3150a	dark green	semierect	medium	medium	weak
3237	middle green	normal	abundant	medium	weak
3332'''	middle green	semierect	abundant	medium	weak
3368''	dark green	semierect	abundant	abundant	weak
3396	dark green	normal	abundant	abundant	weak
3446a	middle green	normal	medium	medium	weak
ACA2000	middle green	normal	medium	medium	strong

Table 4. Qualitative traits evaluated in DR single-crosses during 2007/08.

Hybrid	LC	LP	SP	LPU	LEC
HC14	dark green	normal	abundant	light	weak
HC15	dark green	semierect	abundant	abundant	weak
HC8	dark green	semierect	abundant	light	weak
HC16	dark green	normal	abundant	abundant	strong
HC17	dark green	erect	abundant	abundant	weak
HC18	dark green	normal	abundant	abundant	strong
HC19	middle green	normal	abundant	abundant	weak
HC20	dark green	normal	abundant	abundant	weak
HC21	dark green	semierect	abundant	abundant	strong
HC22	dark green	normal	abundant	abundant	strong
HC23	dark green	normal	abundant	abundant	strong
HC24	dark green	normal	abundant	abundant	weak
ACA2000	verde med	normal	medium	medium	strong

Table 5. Qualitative traits evaluated in waxy single-crosses during 2007/08.

Hybrid	LC	LP	SP	LPU	LEC
HC1	dark green	normal	abundant	light	strong
HC31	dark green	semierect	light	medium	weak
HC32	dark green	normal	abundant	abundant	strong
HC33	dark green	normal	abundant	abundant	weak
HC34	dark green	normal	light	light	weak
HC35	dark green	normal	abundant	abundant	weak
HC36	dark green	semierect	light	light	strong
HC37	dark green	semierect	medium	medium	strong
ACA2000	middle green	normal	medium	medium	strong

Days and heat unit requirements to flowering of quality maize single-crosses developed in Argentina

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It is well known that the number of days necessary to complete each phenological phase varies among environments according to changes in relative humidity, air and soil temperature, solar radiation and photoperiod. Most of the disparities in the number of days to flowering and maturity may be explained on the basis of the diverse temperatures recorded among years and locations. The

influence of temperature on the length of the different stages of maize development was first mentioned by Lehenhauer in 1914. As temperature is the main factor responsible for the interannual variations observed in the length of growth stages and development, several authors created models to calculate the thermal-time (TT) through linear, exponential or more complex equations.

In November 2007, a three-replicate completely randomized block designed field trial was sown at a density of 71,500 plants/ha at Castelar, in the province of Buenos Aires (34°40'00''S, 58°40'00''W; 28masl). Twenty-seven high quality single-crosses, generically named HC, were testcrossed with the dent commercial hybrid ACA 2000 and evaluated last summer (2007/08) for number of days to tasseling (DT), days to silking (DS) and thermal-time, measured as growing-degree days to tasseling (GDDT) and silking (GDDS). The linear method proposed by Gilmore and Rogers in 1958, also known as *modified residual method 10/30*, was used because of its high precision and predictive reliance. This method is based on the amount of energy represented by the sum of degrees centigrade that a plant needs to complete a determined phenological phase and likewise the complete cycle. According to their endosperm characteristics, the materials can be grouped as follows: I) *Modified starch (WAXY)*, II) *High quality protein (HQP)* and III) *Double recessive-o2wx (DR)*. The necessary calculations were performed on the basis of information provided by the Climatology Institute of INTA Castelar obtained through field measurements recorded by an automatic station placed in the location.

Because of the poor correlation between the number of days to flowering and plant growth and development it is not possible to get acceptable results when the genotypes are simply classified by their evolutive cycle, although this may be useful as a guideline. Anyway, a well-fitted classification must be based on the proper measurement of the components of the physical environment that promote variations in the number of days necessary to reach a particular phase.

Table 1 summarizes the information obtained for cycle length to flowering evaluated in the single-cross hybrids tested. The average values show that 96.3% of the genotypes evaluated reached silking (R_1 ; Ritchie & Hanway's scale, 1993) at 63 days or less from emergence (V_E), with a thermal requirement of ≤ 733.2 GDD, calculated according to Gilmore & Rogers. These single-crosses showed a shorter evolutive cycle than the tester ACA 2000, and considering their heat unit requirements to silking, belong to FAO classes 100, 200 and 300-400 (Derieux and Bonhomme, Maydica 35:41-46, 1990). They could be subjectively rated as *ultraprecocious* or *precocious*. The DR hybrids HC15 and HC8 reached silking in 55 days and 631.5 GDD, so they could be classified as FAO 100, or *ultraprecocious*. Silking also occurs at 56-57 days from emergence (650.1-670.1 GDD) in the single-crosses HC14, HC18, HC23, HC24, HC26, HC27, HC31 and HC34, which can also be included in the same class FAO 100.

59.3% of the genotypes reached R_1 between 58 and 70 days from emergence, with a 687.8 to 827.8 GDD, so they correspond to classes FAO 200, FAO 300-400, FAO 500 and FAO 600 and can be classified as *precocious* or *full-season* in relation to their evolutive cycle length. The longest evolutive cycle was observed in the hybrid HC22 (70 days; 771.3 GDD), which was obtained by crossing an early inbred derived from an Argentine maize race

Table 1. Cycle traits measured in different single-crosses tested in Castelar during the summer of 2007/08.

Hybrid	Type	DT	DS	GDDT	GDDS	Interval*	Synchrony
HC5	HQP	56.0	59.0	650.1	702.8	3	good
HC25	HQP	57.0	60.0	670.1	711.2	3	good
HC26	HQP	52.0	56.0	596.6	650.1	4	good
HC27	HQP	54.0	56.0	616.2	650.1	2	very good
HC28	HQP	58.0	62.0	687.8	733.2	4	good
HC29	HQP	54.0	58.0	616.2	687.8	4	good
HC30	HQP	57.0	62.0	670.1	719.2	5	regular
HC14	DR	54.0	57.0	616.2	670.1	3	good
HC15	DR	53.0	55.0	605.7	631.5	2	very good
HC8	DR	52.0	55.0	596.6	631.5	3	Good
HC16	DR	55.0	59.0	631.5	702.8	4	Good
HC17	DR	54.0	58.0	616.2	687.8	4	Good
HC18	DR	55.0	57.0	631.5	670.1	2	very good
HC19	DR	58.0	62.0	687.8	733.2	4	good
HC20	DR	56.0	60.0	650.1	711.2	4	good
HC21	DR	56.0	60.0	650.1	711.2	4	good
HC22	DR	65.0	70.0	771.3	827.8	5	regular
HC23	DR	53.0	56.0	605.7	650.1	3	good
HC24	DR	53.0	57.0	605.7	670.1	4	good
HC1	WAXY	54.0	57.0	616.2	670.1	3	good
HC31	WAXY	53.0	56.0	605.7	650.1	3	good
HC32	WAXY	58.0	63.0	687.8	750.9	5	regular
HC33	WAXY	54.0	58.0	616.2	687.8	4	good
HC34	WAXY	54.0	56.0	616.2	650.1	2	very good
HC35	WAXY	55.0	58.0	631.5	687.8	3	good
HC36	WAXY	57.0	60.0	670.1	711.2	3	good
HC37	WAXY	55.0	58.0	631.5	687.8	3	good
ACA2000	TESTER	57.0	63.0	670.1	733.2	6	wrong
	Env. avg.	55.3	59.0	639.7	694.0		
	s.d.	2.8	3.5	40.0	44.9		
	variance	7.8	12.2	1,603.2	2,015.1		
	CV%*	5.0	5.9	6.3	6.5		
	Min.	52.0	55.0	596.6	631.5		
	Max.	65.0	70.0	771.3	827.8		
	LSD 0,01	1.8	1.9	27.8	31.5		

*= days between tasseling and silking

from the northwestern region and a highly inbred *wx o2* line. Consequently the single-cross HC22 must be classified as class FAO 600 and must be specially considered for cultivation in the northwestern and northeastern areas of Argentina ($\leq 30^\circ$ S). 57.1% of the HQP single-crosses, 66.7% of the DR hybrids and 75.0 % of the waxy single-cross hybrids are precocious or ultraprecocious (FAO 100, FAO 200 and FAO 300-400). No significant differences were found among HQP, DR and waxy hybrids for cycle traits through Student's *t* (see Table 2). The ANOVA detected highly significant differences among hybrids for DT, DS, GDDT and GDDS (see Table 3).

Table 2. Student's *t* significance test for cycle traits of single-crosses evaluated in Castelar during the summer of 2007/08.

Contras	DT	GDDT	DS	GDDS
QPM vs DR	0.53 ns	0.34 ns	0.90 ns	0.95 ns
QPM vs Wx	0.00 ns	0.13 ns	0.00 ns	0.20 ns
DR vs Wx	0.57 ns	0.49 ns	0.92 ns	0.77 ns

ns= non significant; *= significant at 0.05; **= significant at 0.01

Table 3. ANOVA results (mid squares) for cycle traits measured in single-crosses tested in Castelar during the summer of 2007/08.

Variation source	DT	DS	GDDT	GDDS
Hybrid	15.82**	23.26**	3,465.8**	3,964.9**
Replicate	0.23 ns	7.56 ns	196.9 ns	2,454.4 ns

For the hybrids as a group, a highly significant simple correlation index ($r= 0.96$) among days to tasseling and days to silking was found, revealing a good to very good flower synchrony with

intervals of 2 to 3 days between both sexes' maturation (see Table 1 for more details) in most of the genotypes.

A cluster analysis using the algorithm UPGMA and the average linkage method developed in 1958 by Sokal and Michener was run with the purpose of grouping genotypes according to their genotype-environment (GE) interaction on the basis of the data recorded in the field for DS (Figure 1). For example, the single-crosses HC5 and HC16, with 59 days to silking, are very similar in their GE interaction and are placed in the lower part of the dendrogram. A similar situation occurs with the genotypes HC19 and HC28, which reach flowering 62 days after emergence, and are situated in the upper portion of the dendrogram. Four groups can be observed throughout the dendrogram: the two central ones limited by HC8-HC26 and HC1-HC29 include precocious and ultraprecocious materials, whilst the longer cycle hybrids are clustered in the upper group. The long cycle length hybrid HC22 appears on the top of the dendrogram, clearly separated from the rest of the genotypes.

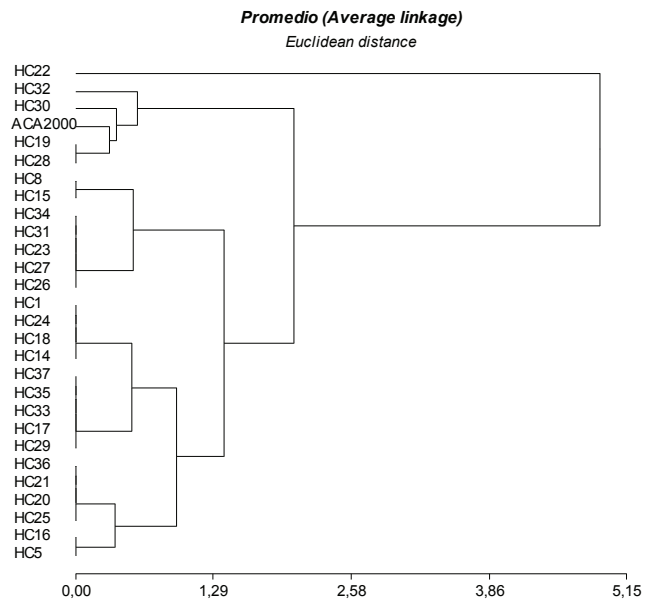


Figure 1. Dendrogram resulting from the cluster analysis of 28 maize genotypes using the UPGMA algorithm on the matrix of Euclidean distances. Only includes data for number of days to silking.

The results obtained reveal the high degree of precocity obtained, even in HQP single-crosses that usually express a long cycle and high thermal requirements to silking. The development of ultraprecocious and precocious materials well-adapted to areas with short summers and a wet autumn will make it possible to increase the economically significant area for corn in Argentina, but in this particular case with high endosperm quality suitable for diverse industrial uses as well as direct feeding. In terms of their degree of precocity, the single-cross hybrids tested could be recommended for late sowing in the northern portion of the Pampeana Area, and in Corn Regions VI, VIII and IX after completion of new field trials.