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# IDENTIFICATION OF SUPERIOR QUALITY PROTEIN MAIZE HYBRIDS FOR DIFFERENT MEGA-ENVIRONMENTS USING THE BIPLOT METHODOLOGY

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**ABSTRACT** - The utilization of site regression models (SREG) on multilocation testing allow the detection of significant differences in the genotype x environment interaction, even though these may not be detected by the analysis of variance (ANOVA). The results can be graphically displayed using the Biplot technique, revealing the additive effects on the genotypes and the genotype x environment interaction across years. Thus, the objectives of this work were to identify mega-environments, superior maize hybrids for each environment and mega-environment, stable maize hybrids with good performance across environments, and the most suitable environments for evaluation as well. A total of 66 field trials were grouped in five sets of experiments. An individual SREG analysis for each set of experiments and their combined analysis were conducted to assist in the graphic representation by the Biplot methodology. Results revealed that the constructed Biplots, graphically allowed the identification of superior maize hybrids, and the proper environments to conduct maize hybrid evaluation trials; however, it was not a reliable option for grouping test-sites in mega-environments.

KEY WORDS: *Zea mays* L.; SREG; QPM; Main components.

## INTRODUCTION

Because of their higher lysine and tryptophan content, QPM varieties and hybrids, are options to improve the nutrition of monogastric organisms such as humans, swine, poultry and fishes, among others. In developing countries where maize is a staple food, this is a very important issue. To contribute towards this effort, CIMMYT and INIFAP, working together, have conducted research to develop, identify and promote quality protein maize (QPM) in different regions of Mexico. The purpose of this article is to present some of the results concerning the performance of QPM hybrids, determined by a series of uniform trials conducted by INIFAP's maize research breeders in tropical and subtropical environments.

The development and identification of new maize hybrids that respond to specific areas in a given environment, is one of the main objectives of a breeding project, which requires multiple environment trials for several years.

It is well recognized that multilocation testing plays a crucial role in the selection of superior stable varieties (or agronomic techniques) which may be later promoted for commercial use (VARGAS *et al*., 1999).

The Biplot GGE technique (graphics of two dimensions where variation due to genotype plus the genotype x environment interaction are taken into account) is a useful tool for the analysis of multilocation trials, since it detects the differences and similarities among environments in their genotype discrimination; the differences and similarities among genotypes in their response to the environment, the superior genotypes and their respective most suitable environment (YAN *et al.*, 2000).

Traditional statistical analysis are not always appropriate for analyzing multilocation uniform trials, since they only have an additive model that identify the genotype x environment interaction as a source of variation, but does not allow its analysis, leading to declarations that such interaction may be regarded as non-significant, when agronomically this can be important (ZOBEL *et al.,* 1988). This is why multiplicative models such as SREG (regression of the environments), that incorporate both additive and multiplicative components which allow to detect significance in the genotype x environment interaction, if it is important.

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Yield estimates are the combined result of the effects of genotypes (G), environments (E) and the genotype x environment interaction (GE); however, only G and GE are important in varietal evaluation and mega-environments identification, thus the Biplot model GGE (G+GE) assists in detecting the performance of each genotype at each testing site (YAN *et al.,* 1999).

CAMARGO *et al.* (2004), used Biplot methodology in 30 environments at the Azuero region in Panamá, to determine similarities and differences among genotypes and environments, and the genotype differential response; the interaction nature and magnitude of any genotype with any locality. Biplot model allows plotting simple genotype-environment interaction graphics, localizing genotypes according to the environment yield responses and positioning the localities according to their discriminatory capacity.

In Mexico, based on yearly rain rate, average temperature and altitude, five principal agro climatic regions (mega-environments) have been recognized for maize adaptation: Hot-humid and sub-humid, irrigated hot-arid, warm sub-humid, high altitude semiarid and high altitude sub-humid. Therefore maize breeding efforts are guided toward the development of maize hybrids and varieties adapted to each environment. However, competitive, stable and performance in successive generations of maize hybrids in more than one of such mega-environment, provides economic feasibility to the entire process. Such understanding contributes also to the identification of environments that render adequate discrimination of hybrid performance. Thus the objectives of this research included the identification of site similarity and the most appropriate testing sites for mega-environment conformation, and the identification of the most stable QPM hybrids with superior yields for each mega-environment.

## MATERIALS AND METHODS

As part of the collaborative activities between INIFAP and CIMMYT, 66 uniform QPM hybrid trials arranged in five sets, were conducted from 1999 to 2001 in the hot humid and sub-humid, the irrigated hot arid, and the warm sub-humid environments. One set was conducted during the fall-winter of 1999-

TABLE 1 - *Quality Protein Maize (QPM) hybrids distributed in five sets of experiments, tested in different sites across Mexico.*

| Num. | Name | Num. | Name | Num. | Name | Num. | Name | Num. | Name |
|---|---|---|---|---|---|---|---|---|---|
| 1† | H - 368 C | 23 | HQ0609 | 45 | HQ460236 | 67 | HQ094602 | T5 | VS 536 |
| 2 | H - 441 C | 24 | H - 551 C | 46 | HQ460209 | 68 | HQ094604 | T6 | Commercial check 1 |
| 3 | H - 371 C | 25 | HQ0519 | 47 | HQ463709 | 69 | HQ094619 | T7 | Commercial check 2 |
| 4 | HQ3736 | 26 | HQ1819 | 48 | HQ364609 | 70 | HQ094636 | T8 | Commercial check 3 |
| 5 | H - 469 C | 27 | H - 365 C | 49 | HQ404609 | 71 | HQ180419 | T9 | Commercial check 4 |
| 6 | HQ0602 | 28 | HQ360246 | 50 | HQ020619 | 72 | HQ180436 | T11 | H - 316 |
| 7 | H - 367 C | 29 | HQ360946 | 51 | H - 519 C | 73 | HQ180446 | T12 | H - 317 |
| 8 | H - 442 C | 30 | HQ020646 | 52 | V - 537 C | 74 | HQ353602 | T13 | REMACO 29 |
| 9 | HQ3602 | 31 | HQ370946 | 53 | V - 538 C | 75 | HQ460602 | T14 | REMACO 31 |
| 10 | H - 443 C | 32 | HQ020946 | 54 | HV - 521 C | 76 | HQ5660132 | T15 | REMACO32 |
| 11 | HQ0605 | 33 | HQ330246 | 55 | VS - 334 C | 77 | HQ56260221 | T16 | H - 358 |
| 12 | HQ1805 | 34 | HQ020933 | 56 | VS - 335 C | 78 | HQ2632 | T17 | H - 359 |
| 13 | HQ3305 | 35 | HQ010402 | 57 | HV - 362 C | 79 | HQ3021 | T18 | Commercial check 5 |
| 14 | HQ3605 | 36 | HQ053602 | 58 | HQ370646 | 80 | HQ3604 | T19 | V - 385 |
| 15 | HQ1006 | 37 | HQ460502 | 59 | HQ56031036 | 81 | HQ3619 | T20 | H - 518 |
| 16 | HQ3306 | 38 | HQ364602 | 60 | HQ010419 | 82 | HQ4604 | T21 | H - 517 |
| 17 | HQ4606 | 39 | HQ330502 | 61 | HQ010446 | 83 | HQ060246 | T23 | H - 520 |
| 18 | HQ5620310 | 40 | HQ374602 | 62 | HQ020936 | 84 | H - 559 C | T24 | REMACO 37 |
| 19 | H - 552 C | 41 | HQ404602 | 63 | HQ024604 | T1‡ | H - 515 | T25 | Commercial check 6 |
| 20 | HQ0204 | 42 | HQ463302 | 64 | HQ024619 | T2 | H - 516 | T26 | REMACO 38 |
| 21 | HQ0504 | 43 | H - 363 C | 65 | HQ041646 | T3 | H - 512 | T27 | Commercial check 7 |
| 22 | H - 554 C | 44 | H - 553 C | 66 | HQ060219 | T4 | H - 513 | T28 | Commercial check 8 |

† Identification number for QPM experimental hybrids;

‡ Identification number for commercial checks hybrids with normal endosperm.

2000 (Set of Experiments-1), two sets in the spring-summer of 1999 (Set of Experiments-2 and 3), and the two remaining sets in the spring-summer of 2000 (Set of Experiments-4) and 2001 (Set of Experiments-5). A total of 84 QPM hybrids and 26 hybrids with normal endosperm, used as reference checks, were included (Table 1). Only 19 hybrids were common to all sets, thus the combined analysis was performed only with this group.

The entries were distributed according to a lattice design with two replicates. Agronomic management was the recommended for each environment.

Measured variables included meaningful plant traits, disease incidence and t $ha^{-1}$ of grain yield. Only this latter trait is considered in this paper. To explain the variation due to genotypes and genotype x environment interaction, the statistical model for the regression on environments (RE) was used.

$$y_{ij} = \mu = \beta_j + \sum_{n=1}^{k} \lambda_n \varepsilon_{in} \eta_{jn}$$

$$\text{with } \lambda_1 \geq \lambda_2 \geq \lambda_3 \ . \ . \ . \geq \lambda_k$$

Where $\mu$ is the effect of the general mean, $\beta$ is the effect of $j^{th}$ environment, $\lambda_n$ is the singular value of $n^{th}$ main component $PC_n$, $\varepsilon_{in}$ and $\eta_{jn}$ are the $i^{th}$ genotype scale in the $j^{th}$ environment scale, respectively for $PC_n$.

The regression analysis results were graphically represented by the Biplot methodology, (YAN *et al.*, 2000), where the first two main components derived from SREG for environments and genotypes were placed as vectors to provide a visual relation among genotypes and environments.

In the Biplot methodology it is possible to identify superior genotypes in terms of the average yield across sites, represented by PC1, and yield stability represented by scales of PC2. Therefore, the ideal genotypes must show high PC1 values (high mean yield) and PC2 values near zero (more stable). YAN *et al.* (2001) indicated that the ideal environment for testing should have high PC1 values (better hybrid discrimination) and PC2 scales near zero (closer representative of the environment mean).

The SREG routines used for the Biplot methodology were developed according to the procedure described by VARGAS and CROSSA (2000) and BURGUEÑO *et al.* (w/d) in the statistical SAS Package (SAS INSTITUTE, 1999).

In the Biplot figure, an angle lower than 90° and higher than 270° between a genotype and a site vectors, points out that the genotype shows a positive response to that environment. A negative response is shown when the angle between the site and the genotype is between 90° and 270°, the cosine of the angle between two environments (or genotypes) brings closer the phenotypic correlation of the two environments (or genotypes), thus an angle of 90° (or <90°) reveals a correlation of 0 (zero), an angle of 180° a correlation of -1 and an angle of 0° indicates a correlation of +1 (BURGUEÑO *et al.*, w/d).

## RESULTS AND DISCUSSION

The ANOVA of the five sets of experiments (Table 2) revealed significant differences among genotypes at the $\alpha$ level of 0.01 and for the genotype x environment interaction. The SREG also detected significant differences among the principal two main components (Table 3). The variation due to sites ranged between 84.0 and 89.8%, proportionally being the largest and justifying the use of SREG model. This model only uses the variation due to genotypes and their interaction with the environments (G + GE). Similarly, the combined analysis also detected significant differences and the source of variation due to trials and sites, across sets of experiments was greater than that presented by the other sources of variation.

TABLE 2 - *Analysis of variance of five sets of QPM experimental hybrids.*

| Set of Exps. | Source of variation | D.F. | Sums of Squares | % of H+ S + HS | Mean Square |
|---|---|---|---|---|---|
| 1 | S | 10 | 6.479 x $10^9$ | 89.5 | 6.479 x $10^{8**}$ |
| | H | 35 | 1.004 x $10^8$ | 1.4 | 2.869 x $10^{6**}$ |
| | H*S | 350 | 6.555 x $10^8$ | 9.1 | 1.872 x $10^{6**}$ |
| | e | 275 | 1.833 x $10^8$ | | 6.666x $10^5$ |
| 2 | S | 12 | 1.922 x $10^{10}$ | 89.8 | 1.601 x $10^{9**}$ |
| | H | 63 | 8.027 x $10^8$ | 3.7 | 1.274 x $10^{7**}$ |
| | H*S | 756 | 1.387 x $10^9$ | 6.5 | 1.835 x $10^{6**}$ |
| | e | 765 | 6.348 x $10^8$ | | 8.299 x $10^5$ |
| 3 | S | 5 | 6.469 x $10^9$ | 88.9 | 1.293 x $10^{9**}$ |
| | H | 48 | 3.176 x $10^8$ | 4.4 | 6.618 x $10^{6**}$ |
| | H*S | 240 | 4.879 x $10^8$ | 6.7 | 2.033 x $10^{6**}$ |
| | e | 216 | 2.462 x $10^8$ | | 1.140 x $10^6$ |
| 4 | S | 17 | 9.294 x $10^9$ | 84.8 | 5.467 x $10^{8**}$ |
| | H | 35 | 4.840 x $10^8$ | 4.4 | 1.383 x $10^{7**}$ |
| | H*S | 595 | 1.178 x $10^9$ | 10.8 | 1.980 x $10^{6**}$ |
| | e | 667 | 8.017 x $10^8$ | | 1.202 x $10^6$ |
| 5 | S | 7 | 4.318 x $10^9$ | 84.0 | 6.169 x $10^{8**}$ |
| | H | 63 | 1.821 x $10^8$ | 3.5 | 2.891 x $10^{6**}$ |
| | H*S | 411 | 6.425 x $10^8$ | 12.5 | 1.456 x $10^{6**}$ |
| | e | 392 | 2.878 x $10^8$ | | 7.344 x $10^5$ |
| Comb. | E | 4 | 3.929 x $10^9$ | 16.1 | 9.822x $10^{8**}$ |
| | S/E | 51 | 1.833 x $10^{10}$ | 75.3 | 3.594 x $10^{8**}$ |
| | H | 18 | 1.760 x $10^8$ | 0.7 | 9.778 x $10^{6**}$ |
| | E*H | 72 | 3.359 x $10^8$ | 1.4 | 4.665 x $10^{6**}$ |
| | S*H/E | 918 | 1.573 x $10^9$ | 6.5 | 1.714 x $10^{6**}$ |
| | e | 1160 | 1.247 x $10^9$ | | 1.075 x $10^6$ |

** Significance level 0.01 respectively; E, S, H, H*S, S/E, E*H, S*H/E are the sources of variation from experiments, sites, hybrids, sites x hybrid, site across experiments, experiments x hybrids and hybrids x sites across experiments; Comb., combined analysis of the hybrids tested across experiments and sites.

### *Set of experiments 1*

Figure 1 illustrates the performance of 36 hybrids tested at 11 sites, based on the mean hybrid grain yields. The sites could be grouped geographically in 4 mega-environments. It was also possible to identify the hybrids with superior average performance for the test sites that integrate each mega-environment (Table 4). The sites grouping according to their mega-environment did not coincide with the traditional classification, since the hot arid, warm sub-humid sites, as well as the hot arid and hot humid and sub-humid sites group together in a single mega-environment.

It is important to point out that the same site has contrasting differences in the fall-winter versus the spring-summer cycle. Therefore site grouping according to the traditional classification does not apply. The traditional clustering and the regression analysis does not coincide, since such analysis divides the sites (environment) in four mega-environments.

Using the method of CROSSA *et al.* (2002) the five superior hybrids at each location were identified (Table 5). These authors indicate that the performance of a hybrid in a given location is estimated by the orthogonal projection of the hybrids vector on the line determined by the direction of the vector of that location; in other words, if the vector lines location is taken into account, the hybrid response to that site is approximately the distance of the segment of that line extended from the origin to the point, where the line can be perpendicularly intercepted by the line drawn from the hybrids vector.

The identification of superior hybrids at each mega-environment is based on their average performance, taking into account all sites belonging to that mega-environment; therefore, the best hybrids at a location are not necessarily the same as those of the mega-environment where that location was included.

Following the YAN *et al.* (2000) criteria, the hybrids that showed the best positive response to their environments (Table 10) were those that occupy the polygon's vertexes on the right hand side of the graphic (Fig. 1). These hybrids were: 7(H-367C), 24(H-551C), 45(HQ460236) and T2(H-516); similarly, the hybrids that occupy the vertexes to the left hand side of the graphic (Fig. 1) were those with the largest negative response. Such hybrids are the following: 15(HQ1006), 18(HQ5620310), 35(HQ010402) and T20(H-518).

TABLE 3 - *Statistical significance of the two main components (PC) for each set of experiments.*

| Set of Exps. | $\lambda^2$ | % of H + HS | Degrees of freedom | Mean Square |
|---|---|---|---|---|
| 1 | | | | |
| PC1 | 2.938 x $10^8$ | 32.63 | 43 | 6.834 x $10^{6**}$ |
| PC2 | 2.286 x $10^8$ | 25.39 | 41 | 5.577 x $10^{6**}$ |
| $\varepsilon$ | | | 275 | 6.666 x $10^5$ |
| 2 | | | | |
| PC1 | 1.188 x $10^9$ | 45.83 | 74 | 1.605 x $10^{7**}$ |
| PC2 | 4.539 x $10^8$ | 17.51 | 72 | 6.305 x $10^{6**}$ |
| $\varepsilon$ | | | 756 | 8.299 x $10^5$ |
| 3 | | | | |
| PC1 | 4.753 x $10^8$ | 45.96 | 52 | 9.141 x $10^{6**}$ |
| PC2 | 2.042 x $10^8$ | 19.74 | 50 | 4.084 x $10^{6**}$ |
| $\varepsilon$ | | | 216 | 1.140 x $10^6$ |
| 4 | | | | |
| PC1 | 8.898 x $10^8$ | 48.83 | 51 | 1.744 x $10^{7**}$ |
| PC2 | 1.874 x $10^8$ | 10.28 | 49 | 3.825 x $10^{6**}$ |
| $\varepsilon$ | | | 667 | 1.202 x $10^6$ |
| 5 | | | | |
| PC1 | 4.682 x $10^8$ | 44.92 | 69 | 6.786 x $10^{6**}$ |
| PC2 | 1.644 x $10^8$ | 15.77 | 67 | 2.454 x $10^{6**}$ |
| $\varepsilon$ | | | 392 | 7.344 x $10^5$ |
| Comb. | | | | |
| PC1 | 3.308 x $10^8$ | 28.59 | 50 | 6.616 x $10^{6**}$ |
| PC2 | 1.914 x $10^8$ | 16.550 | 48 | 3.989 x $10^{6**}$ |
| $\varepsilon$ | | | 1160 | 1.075 x $10^6$ |

** Significance level: 0.01, $\lambda^2$ is the eigen value of each main component;
% of H + HS is the percentage of variation.

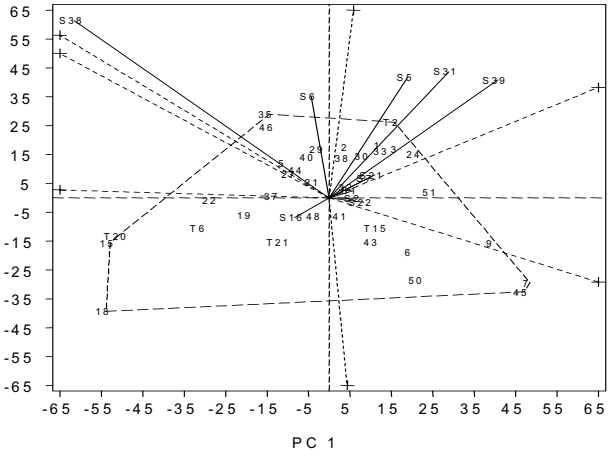


FIGURE 1 - Set of experiments 1; Biplot of hybrids and test sites. Fall-winter, 1999.

TABLE 4 - *Clustering of test sites in mega-environments and superior hybrids.*

| Set of Exps. | Superior Hybrids | Groups of sites | Superior hybrids in each mega-environment | Climatic domain |
|---|---|---|---|---|
| 1 | 35 | S6, S38 | 5, 21, 27, 29, 40, 44, 46, | WSH |
| | T2 | S5, S7, S21 S31, S39 | 1, 2, 3, 24, 30, 32, 33, 38 | WSH |
| | - | S1, S2, S22 | 9, 51 | WSH |
| | 15, 18, T20 | S16 | 19, 22, 48, T6, T21 | WSH |
| 2 | 18 | S13, S44 | 5, 11, 14, 15, 17, 19, 22, 23, 25, 27, 28, 31, 43, 48, 49, 50, 51, T2, T5 | HHSH, HA |
| | 3 | S1, S2, S5, S7, S16, S22, S41, S45, S46, S47 | 1, 2, 6, 7, 29, 32, 33, 36, 45, 46, T8 | HA, HHSH, |
| | - | S42 | 4, T9 | HA |
| 3 | 3, T16, T17 | S36 | 5, 17, 27, 33, 39, 47, 49, 51, T9, T11, T13, T14, T15, T19, T29 | WSH |
| | T18 | S8, S32, S33, S43 | 2, 7 | WSH |
| | 38 | S18 | 1, 30, 37, 41, 45, 48 | WSH |
| 4 | 22, 2 | S7, S21, S31, S40 | 9, 19, 48, 43, T8, 1, 5, 44, 4, 30 | HHSH |
| | T23 | S2, S6, S30, S39, | T2 | HHSH |
| | - | S3, S16 | T24 | HHSH |
| | T25 | S1, S12, S17, S26, S27, S28, S32 | 3, 6, 24, 29, 32, 35, 37, 38, 46 | HHSH, HA, WSH |
| | 33 | S4 | 28, 39, 41 | WSH |
| 5 | T26 | S1, S6, S9, S16, S30 | 4, 9, 32, 35, 40, 45, 60, 62, 65, 67, 74, 75, T23, T24, T27. | HHSH, WSH |
| | T9 | S18, S32 | 28, 33, T2 | WSH |
| | 3, 34 | S26 | 2, 27, 29, 48, 63, 73, 83 | HA |
| Comb. | 7 | S22 | 43, 44 | HHSH |
| | 9, 45 | S1, S2, S7, S13, S16, S30, S39, S41, S42 | – | HHSH, HA |
| | 3, 8 | S3, S4, S5, S6, S8, S12, S17, S18, S21, S26, S27, S28, S31, S32, S33, S40, S43, S44, S46, S47 | 2, 33, 38, 44 | HHSH, WSH, HA |
| | 46 | S36, S38, S45 | 1, 29, 32, 40 | WSH, HA, HHSH |
| | 27, 51 | S9 | 5, 48 | WSH |

HHSH = Hot Humid Sub-Humid; HA = Hot Arid; WSH = Warm Sub-Humid.

***Set of experiments 2***

The analysis revealed that the 64 hybrids included in this trial and tested at 13 sites (Fig. 2) could be clustered into three mega-environments. The following hybrids revealed the largest positive response to the environments: 3(H-371C), 8(H-442C), 38(HQ364602), and 20(HQ0204); while 10(H-443C), 12(HQ1805), 18(HQ5620310), 39(HQ330502) and 53(V-538C) revealed the greater negative response (Table 10) and therefore the least recommendable.

In Table 6, the five superior hybrids for each one of the test sites are given. Table 4 provides the site clustering for the mega-environments and the hybrids that on the average were the best yielders at the sites that belong to that mega-environment. Using SREG did not match with the traditional approach, since sites commonly separated in hot humid and sub-humid, and hot arid (irrigated) were clustered in the same mega-environment.

***Set of experiments 3***

The performance of 49 hybrids across six test sites, is shown in Fig. 3. The three mega-environments that were identified did not coincide with the traditional classification, since the test sites used in this trial belong to the warm sub-humid environment (Table 4). The performance of the best hybrids at each one of the test sites is given in Table 7. Hy-

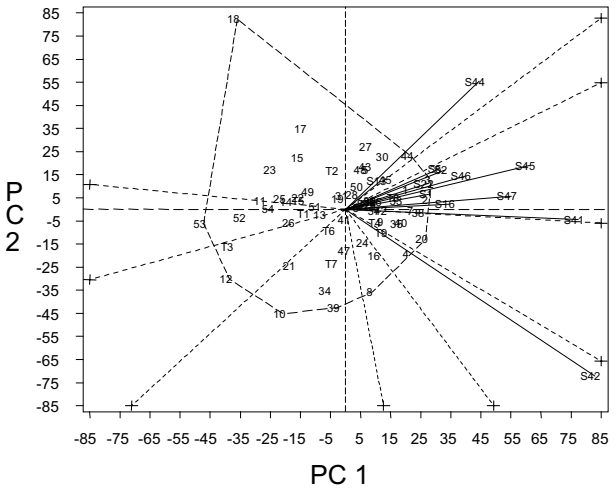


FIGURE 2 - Set of experiments 2; Biplot of hybrids and test sites. Spring-summer, 2000.

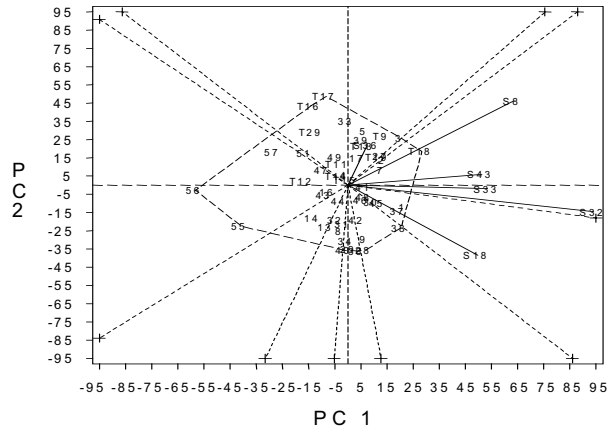


FIGURE 3 - Set of experiments 3; Biplot of hybrids and test sites. Spring-summer, 2000.

brids with the most positive response across sites were: 3(H-371C), 28(HQ360246), 29(HQ360946), 36(HQ053602), 38(HQ364602), 40(HQ374602) and T18(Commercial check 5). Those that showed a negative response were: 55(VS-334C), 56(VS-335C), T16(H-358) and T17(H-359) (Table 10).

### *Set of experiments 4*

This set included 36 hybrids was tested at 18 sites. The results from the analysis are presented in Fig. 4. Two hybrids, 2(H-441C), 33(HQ330246) and two checks, T23(H-520) and T25 (Commercial check 6), gave the best positive response, while hybrids 22(H-554C), 27(H-365C) and 51(H-519C) showed the largest negative response (Table 10).

TABLE 5 - *Superior QPM hybrids in Set of experiments 1, which was conducted in the fall-winter cycle of 1999-2000.*

| Site Code | Site | Superior 5 hybrids |
|---|---|---|
| S1 | Río Bravo, Tamps. | T2, 24, 3, 1, 33 |
| S2 | Tampico, Tamps. | 7, 45, 9, 51, 24 |
| S5 | Santiago Ixcuintla, Nay. | T2, 24, 3, 1, 33 |
| S6 | Apatzingán, Mich. | 35, 46, T2, 29, 2 |
| S7 | Tecomán, Col. | T2, 24, 3, 1, 33 |
| S16 | Uxmal, Yuc. | 18, 15, T20, T6, 22 |
| S21 | Huimanguillo, Tab. | T2, 24, 3, 1, 33 |
| S22 | Iguala, Gro. | 7, 45, 9, 51, 24 |
| S31 | Zacatepec, Mor. | T2, 24, 3, 1, 33 |
| S38 | Costa de Guerrero, Gro. | T20, 15, 35, 46, 22 |
| S39 | Champusco, Pue. | T2, 24, 3, 1, 33 |

TABLE 6 - *Superior QPM hybrids in Set of experiments 2, which was conducted in hot sites in the spring-summer of 1999.*

| Site Code | Site | Superior 5 hybrids |
|---|---|---|
| S1 | Río Bravo, Tamps. | 3, 2, 20, 38, 44 |
| S2 | Tampico, Tamps. | 3, 2, 44, 38, 20 |
| S5 | Santiago Ixcuintla, Nay. | 3, 2, 44, 38, 20 |
| S7 | Tecomán, Col. | 3, 2, 44, 38, 20 |
| S13 | Ocozocuautla, Chis. | 44, 3, 2, 30, 1 |
| S16 | Uxmal, Yuc. | 3, 2, 20, 38, 7 |
| S22 | Iguala, Gro. | 3, 2, 44, 38, 20 |
| S41 | Valle del Fuerte, Sin.[1]† | 3, 2, 20, 38, 7 |
| S42 | Valle del Fuerte, Sin.[2] | 20, 4, 8, 38, 2 |
| S44 | Valle del Yaqui, Son. | 44, 3, 2, 30, 27 |
| S45 | Valle del Yaqui, Son.[2] | 3, 2, 44, 20, 38 |
| S46 | Valle de Culiacán, Sin.[1] | 3, 2, 44, 20,38, |
| S47 | Valle de Culiacán, Sin.[2] | 3, 2, 20, 38, 7 |

† [1, 2] Trials conducted at the same site but in different planting dates.

TABLE 7 - *Superior QPM hybrids in Set of experiments 3, which was conducted in the warm sites in the spring-summer of 1999.*

| Site Code | Site | Superior 5 hybrids |
|---|---|---|
| S8 | Morelia, Mich. | T18, 3, T9, 5, T17 |
| S18 | Pabellón, Ags. | 38, 1, 37, 28, 36 |
| S32 | Celaya, Gto. | T18, 38, 1, 37, 3 |
| S33 | Calera, Zac. | T18, 38, 1, 37, 3 |
| S36 | Cd. Guzmán, Jal. | T17\|, T16, 33, 3, 5 |
| S43 | Cortazar, Gto. | T18, 3, 1, 37, 38 |

TABLE 8 - *Superior QPM hybrids in Set of experiments 4, which was conducted in the hot and warm sites in the spring-summer of 2000.*

| Site Code | Site | Superior 5 hybrids |
|---|---|---|
| S1 | Río Bravo, Tamps. | T25, 3, T23, T2, T24 |
| S2 | Tampico, Tamps. | 2, T2, 3, T24, 44 |
| S3 | Ebano, S.L.P. | T2, 2, T25, 3, T24 |
| S4 | Tlajomulco, Jal. | 33, T25, 39, 28, 35 |
| S6 | Apatzingán, Mich. | T2, 2, T25, 3, T24 |
| S7 | Tecomán, Col. | 22, 2, T23, T2, 44 |
| S12 | Villa Flores, Chis. | T25, 3, T23, T2, T24 |
| S16 | Uxmal, Yuc. | T25, T23, 3, T2, 2 |
| S17 | Edzna, Camp. | T25, 3, T23, T24, 35 |
| S21 | Huimanguillo, Tab. | 2, T2, 44, 1, T8 |
| S26 | Obregón, Son. | T25, 3, T2, T24, 35 |
| S27 | Valle del Fuerte, Sin. | T25, 33, 3, 35, T23 |
| S28 | Valle de Culiacán, Sin. | T25, 33, 3, 35, T23 |
| S30 | Loma Bonita, Oax. | 2, T2, T24, 44, 3 |
| S31 | Zacatepec, Mor. | 22, T23, 9, 2, 1 |
| S32 | Celaya, Gto. | T25, 3, T23, T24, 35 |
| S39 | Champusco, Pue. | 2, T2, 3, T24, 44 |
| S40 | Izúcar de Matamoros, Pue. | 22, 2, T23, T2, 44 |

TABLE 9 - *Superior QPM hybrids in Set of experiments 5, which was conducted in the hot arid and warm sites in the spring-summer of 2001.*

| Site Code | Site | Superior 5 hybrids |
|---|---|---|
| S1 | Río Bravo, Tamps. | T26, T24, T27, T9, 24 |
| S6 | Apatzingán, Mich. | T26, T24, T27, T9, 24 |
| S9 | Puebla, Pue. | T26, T24, T27, T9, 24 |
| S16 | Uxmal, Yuc. | T26, T24, T27, T9, 24 |
| S18 | Pabellón, Ags. | T9, 3, 29, T26, 34 |
| S26 | Obregón, Son. | 3, 34, 29, 31, 5 |
| S30 | Loma Bonita, Oax. | T26, 24, T24, T23, T27 |
| S32 | Celaya, Gto. | T9, 3, T26, 29, 34 |

The test sites represent five mega-environments. For each one, the superior hybrids are provided, as well as those that on the average had the highest yields across all sites that belong to each mega-environment (Table 4). The site allocation to each one of the mega-environments did not coincide with the traditional clustering, since there were mega-environments that included sites (regions) that belong to the hot humid and sub-humid, hot arid and warm sub-humid environments. Table 8 presents the best hybrids at each testing site.

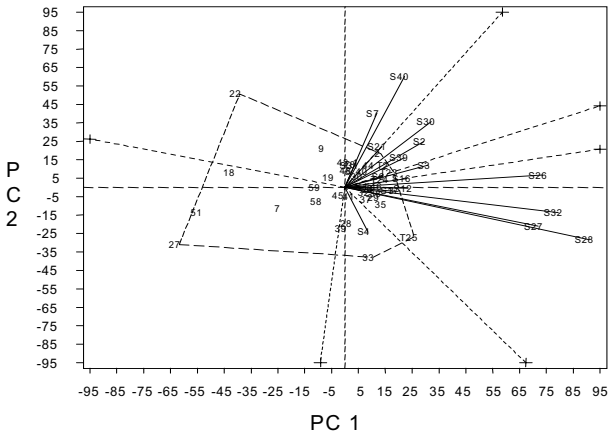


FIGURE 4 - Set of experiments 4; Biplot of hybrids and test sites. Spring-summer, 2001.

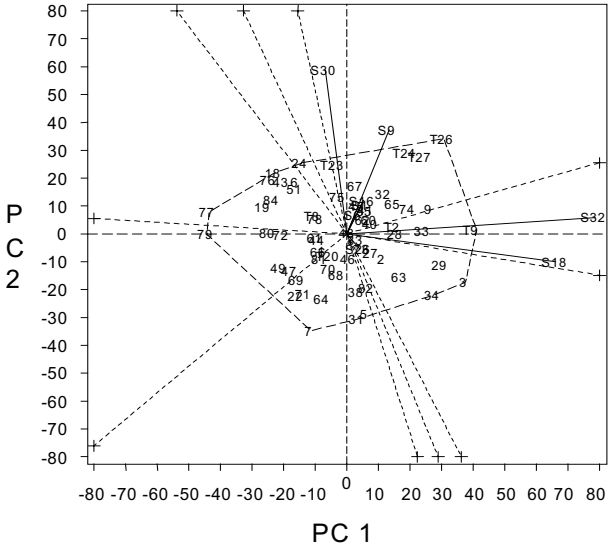


FIGURE 5 - Set of experiments 5; Biplot of hybrids and test sites. Spring-summer, 2001.

### *Set of experiments 5*

The performance of 64 hybrids and eight test sites (Fig. 5) could be subdivided into three mega-environments, each one formed with similar sites, and the highest yielding hybrids across sites that belong to each mega-environment. As in previous sets of experiments, the mega-environment division did not coincide with the traditional site clustering, since the hot humid, hot sub-humid and warm sub-humid sites were grouped in the same mega-environment.

This was also true for the hot arid and warm sub-humid (Table 4) sites. In Table 9, the superior hybrids for each site are given.

The hybrids that showed the best positive response to the test sites were: 3(H-371C), 31(HQ370946), 34(HQ020933), T26 (REMACO 38), T28 (Commercial check 8). The hybrids with the greater negative response were (Table 10): 7(H-367C), 18(HQ5620310), 24(H551C), 77(HQ5626221) and 79(HQ3021).

### *Combined analysis*

Because not all tested hybrids were included in the five experiments, the combined analysis was conducted only with the 19 hybrids common to all trials. This set was tested at 34 sites.

The analysis grouped the sites in five mega-environments (Fig. 6). For each group, the superior hybrids and those that performed the best across test sites in the mega-environment, are given. Again, the test site clustering did not match the traditional grouping since the sites belonging to each one of the three climatic regions were grouped in the same mega-environment.

The hybrids that revealed the greater positive response were: 3(H-371C), 8(H-442C), 46(HQ460209). Those with a negative response were: 7(H-367C), 9(HQ3602), 27(H-365C), 45(HQ460236) and 51(H-519C) (Table 10).

The sites regression analysis from each one of the five sets of experiments revealed the clustering of the climatic regions in mega-environments did

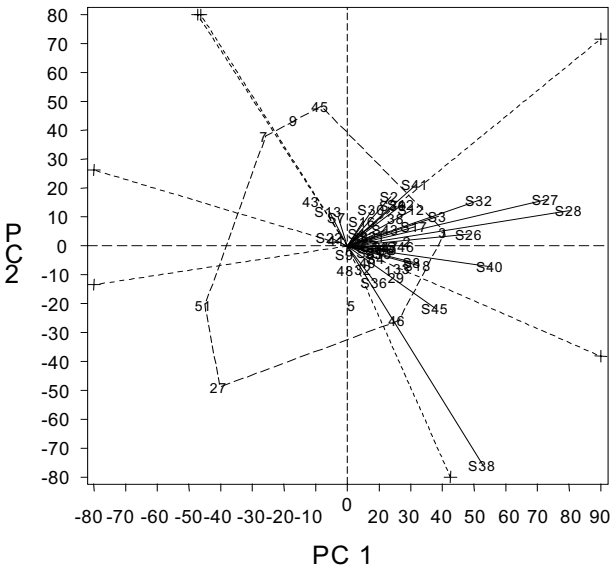


FIGURE 6 - Combined analysis; Biplot of hybrids and test sites.

TABLE 10 - *Hybrids with greater positive or negative response to test environments.*

| Set of Exps. | Positive | Negative |
|---|---|---|
| 1 | 7, 24, 45, T2 | 15, 18, 35, T20 |
| 2 | 3, 8, 18, 20 | 10, 12, 18, 39, 53 |
| 3 | 3, 28, 29, 36, 38, 40, T18 | 55, 56, T16, T17 |
| 4 | 2, 33, T23, T25 | 22, 27, 51 |
| 5 | 3, 31, 34, T26, T28 | 7, 18, 24, 77, 79 |
| Comb. | 3, 8, 46 | 7, 9, 27, 45, 51 |

TABLE 11 - *Optimum test sites for QPM hybrids evaluation.*

| Set of Exps. | Site Code | Site |
|---|---|---|
| 1 | S2 | Tampico, Tamps. |
| | S22 | Iguala, Gro. |
| 2 | S16 | Río Bravo, Tamps. |
| | S41 | Valle del Fuerte, Sin.[1]† |
| | S47 | Valle de Culiacán, Sin.[2] |
| 3 | S32 | Celaya, Gto. |
| | S33 | Calera, Zac. |
| | S43 | Cortazar, Gto. |
| 4 | S26 | Obregón, Son. |
| | S32 | Celaya, Gto. |
| 5 | S18 | Pabellón, Ags. |
| | S32 | Celaya, Gto. |
| Comb. | S26 | Obregón, Son. |
| | S28 | Valle de Culiacán, Sin. |
| | S40 | Izucar de Matamoros, Pue. |

† [1, 2] Trial conducted at the same site in different planting dates.

not coincided with the traditional approach. This may be attributed to the fact that the hybrids used to structure the trials were derived from germplasm already adapted to each of the hot humid, sub-humid and warm sub-humid climatic domains, but hybrids adapted to the three domains were not included. In addition, the average hybrid yields were used to define the mega-environments, however, such hybrids were different than those from each experiment, and their performance influenced how the mega-environments were clustered in each experiment.

Biplot analysis (YAN *et al.,* 2000) of trials con-

TABLE 12 - *Stable hybrids across sites with positive response.*

| Set of Exps. | Hybrid number | Name |
|---|---|---|
| 1 | 51 | H – 519 C |
| 2 | 6, 7, 29, 32, 36, 37, 38, 42, 46, | HQ0602, H - 367C, HQ360946, HQ020946, HQ053602, HQ460502, HQ364602, HQ463302, HQ460209 |
| 3 | 41, T15 | HQ404602, REMACO32 |
| 4 | 3, 6, 24, 32, 46 | H - 371 C, HQ0602, H - 551 C, HQ020946, HQ460209 |
| 5 | 28, 33, 48, 83, T2, T9 | HQ360246, HQ330246, HQ364609, HQ060246, H - 516, commercial Check 4 |
| Comb. | 2, 3, 44 | H - 441 C, H - 371 C, H - 553 C |

ducted in different years revealed that site clustering changed across years, and in most cases, mega-environments as indicated by the clustering of sites.

***Test environments***

The sites where hybrid performance was not influenced by the interaction with the environments were identified (YAN *et al.,* 2001). These authors point out that the main effect of the environment (PC1) allowed sites to separate hybrids in terms of better general adaptation. In other words, sites with large primary effects may identify hybrids with better adaptation. The secondary effect of the environment (PC2) indicates the tendency of each site to interact with the hybrids (GE). Hybrids selected with large secondary effects at sites may be regarded as specific for those domains, but fail in their general adaptation.

Therefore, selection for stable and high yielding hybrids, the optimum test environment should be the one with large primary effects and secondary effects near zero. The most appropriate test sites to conduct evaluations for each one of the experiments are given in Table 11. The better sites of evaluation in each of the five sets of experiments were: Tampico e Iguala for the sets of experiments 1; Valle del Fuerte, Culiacan and Rio Bravo for the set of experiments 2; Calera, Celaya and Cortazar for the set of experiments 3; Obregon and Celaya for the set of experiments 4, Pabellon and Celaya for the set of experiments 5; and Obregon, Izucar and Culiacan for the combined analysis. None of these sites were common to all sets of experiments, which prevented comparisons among sets of experiments.

It is recognized that multilocation hybrid testing brings up research costs in hybrid development. Therefore selection of suitable sites such as Celaya, Obregon (Yaqui Valley) and Culiacan, may contribute to cutting down number of test locations, and reduce costs of sacrificing accuracy in the detection of the superior hybrids. However, the Celaya site was not included in the combined analysis, because none of the 19 hybrids common to all trials were present at this site. This is a short coming of the regression model (SREG), because graphic construction is based on average hybrid grain yield; thus the interpretation of results may change drastically by the inclusion or omission of some hybrids. The information presented here need to be verified.

***Stable hybrids across test sites***

Table 12 presents the stable hybrids in each trial set and in the combined analysis that had PC2 values approaching zero. Because each set of experiments was conducted at different sites and hybrid stability is based on the across site yield, it was not possible to determine the appropriateness of the methodology across sets of experiments.

## CONCLUSIONS

The Biplot methodology effectively allowed the recognition of the superior hybrids across sites in each evaluation year. However, this is not a reliable model to cluster sites in mega-environments, since such clustering was not consistent across years. This is because of allotment to mega-environments is done considering only the hybrid average yield, and the clustering of sites in mega-environments changes when geographic, climatic and edaphic factors are not taken into account.

In order to determine with accuracy the efficiency of the Biplot approach in the identification of mega-environments, uniform sets of the same hybrids, including hybrids adapted to each agro climatic domain, should be conducted for at least two consecutive years.

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