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# Combining abilities and heterotic groups in *Pisum sativum* L.

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**Abstract**

The objective of this research was to investigate the use of heterosis and estimates of the general combining ability (GCA) and specific combining ability (SCA) for yield and the yield-related traits for identifying suitable parents and forming heterotic groups for pea- breeding programs. Seventy-six $F_1$ hybrids derived from crosses between nineteen female lines and four male testers were evaluated during two seasons. Estimates of variance due to GCA and SCA effects and their relationship revealed predominantly additive effects for all traits. Parents with higher GCA values were 'ZAV20' (female parent) and 'ZAV23' (male parent).The cross 'ZAV5 x ZAV23' showed the highest value for seed yield. Days to flowering and number of seeds per plot were the variables with the highest values for broad and narrow-sense heritability (0.93 and 0.65, respectively), indicating that these traits are highly heritable. The highest best parent heterosis for seed yield was observed in the 'ZAV17 x DDR14' hybrid. Four heterotic groups were formed and validated by estimating the intra and inter group heterosis.

**Keywords:** *Pisum sativum* L, line x tester, seed yield, combining ability, heterosis.
**Abbreviations:** GCA_general combining ability, SCA_specific combining ability, BPH_Best Parent Heterosis, NP_number of pods, Y_yield, NS_number of seeds per plot, WS_weight of 100 seed, DF_Number of days to flowering.

## Introduction

The pea (*Pisum sativum* L.) is an annual grain legume of the Fabaceae family which originated in Southwest Asia. Wild field pea can still be found in Afghanistan, Iran and Ethiopia. It is one of the four most important cultivated legumes along with soybean, groundnut and beans (Smýkal et al. 2012). Because of its high protein level (20-30%) (Ceyhan et al., 2008), and the increasing demand for protein-rich raw materials for animal feed or intermediate products for human nutrition, there is rising interest in this crop as a protein source (Santalla et al., 2001). However, the relatively narrow gene pool and the use of a small number of varieties as parents by competing breeding programs have led to a low genetic diversity among pea cultivars (Espósito et al., 2007).

Knowledge of the combining abilities of inbred lines to be used as parents of hybrids is very important for breeding programs. Combining ability analysis improves the selection and assessment of parental inbred lines, thus increasing the opportunity of selecting excellent crosses. Therefore, knowledge of combining ability is essential for the selection of suitable parents with different genes to produce transgressive segregation. Lines with high combining ability produce hybrids with higher yield than lines with low combining ability (Turbin et al., 1974). Thus, breeding programs of varieties and lines should be developed on the basis of high combining ability values. Combining ability analysis allows estimating the effects of combining ability, and it aids in the selection of desirable parents for heterotic crosses. Line × tester analysis (Kempthorne, 1957) provides information about the effects of general combining ability (GCA) and specific combining ability (SCA) of parents, and is also helpful in estimating various types of gene actions (Griffing 1956; Baker 1978; Falconer and Mackay, 1996). The estimation of additive and non-additive gene action through combining ability analysis could be useful for isolating pure lines among the progenies of the good hybrids (Stuber 1994). The ability to categorize the pea germplasm into different heterotic groups and to reliably predict the magnitude of heterosis will have a significant impact on breeding programs efficiency. The expression of heterosis depends on the differences in the gene frequencies of the parental stocks, whether they are cultivars or inbred lines. When a hybrid has high heterosis, it is assumed that the two parents are more genetically diverse than the parents of hybrids with little or no heterosis (Hallauer and Miranda, 1988). Nevertheless, the opposite is not true, i.e. the lack of heterotic response cannot be used to infer lack of genetic divergence (Cress, 1966). A heterotic group is a set of lines or cultivars that traces back to a common origin and display similar combining ability when crossed with lines from different genetic backgrounds (Dubreuil et al., 1996). Heterotic grouping means identifying germplasm groups that are genetically distinct from each other and that produce superior hybrids when crossed. Crossings between representative individuals of different heterotic pools maximize heterozygosity, heterosis and yield stability of the new cultivars. Heterotic groups identified via diversity analysis are validated through multi-location evaluation of intra-pool and inter-pool crosses. This enables identification of the optimal genetic distance among parental materials for attaining maximal heterosis. Several studies have evaluated the combining abilities in pea (Gritton, 1975; Singh and Singh, 1990; Sarawat et al., 1994; Sharma et al., 1999; Ceyhan and Avci, 2005 - 2008; Espinosa y Ligarreto, 2005; Borah, 2009; Jyothula and Guttala, 2009; Kalia and Sood,

2009; Bisht and Singh, 2011), However, no studies about the formation of heterotic groups on the basis of combining abilities have been published to date for pea. The purposes of this study were (i) to estimate general and specific combining ability values for yield, yield-related traits and morphological traits among nineteen genotypes used as female parents and four testers; (ii) to identify appropriate parents and crosses for the traits evaluated to assess their potential use in pea breeding programs; (iii) to estimate heritability, and (iv) estimate the heterosis for yield of 76 $F_1$ populations developed by line × tester system to form heterotic groups.

**Results and discussion**

***General combining ability (GCA) and specific combining ability (SCA)***

Combining ability describes the breeding value of parental lines to produce hybrids, and thus helps in the identification of parents with high GCA and parental combinations with high SCA (Sprague and Tatum 1942; Griffings 1956). Combining ability analysis is a powerful tool to select good combiners, and for choosing appropriate parental material in crop breeding programs. The *per se* performance of a given parent does not necessarily mean that it is a good or poor combiner. Therefore, gathering information on nature of gene effects and their expression in terms of combining ability is necessary. Higher SCA values for a trait indicate dominance genetic effects, and higher GCA effects indicate a greater role of additive genetic effects controlling that trait. If both the GCA and SCA values are not significant, epistatic gene effects may play an important role in determining these traits (Fehr 1993). Significance of GCA and SCA mean squares for traits at each and across environments indicates the importance of both additive and non-additive genetic effects in the inheritance of these traits. Highly significant GCA variances were found for NS and DF in the 19 lines, and highly significant GCA variances for NP, NS and DF were found in the testers. Highly significant SCA variances for all characters except NP and DF were found. Testers used in this study are varieties of different geographical origins, 'DDR 14' from India, 'Come' from France, 'AMA' from the USA, and 'ZAV23' from a local breeding program. Estimates of GCA of the 23 genotypes for five traits showed that 'ZAV25' was the best combiner for, NP; 'ZAV20' for grain yield (Y); 'C2001' for NS; 'VIP' for DF and 'KEOMA' for WS. 'ZAV2'3 was the best tester for NP and Y, 'DDR14' for NS and DF, and 'COME' for WS (Table 1). The estimates of SCA of 76 crosses for the five traits are presented in Table 2. The cross 'KEOMA x DDR14' exhibited high SCA effects for NP and NS. The cross 'ZAV5 x ZAV23' was good for Y. 'ZAV17 x DDR14' and 'KEOMA x COME' were good combiners for DF and WS respectively. The high SCA value of these hybrids for the NP, NS, and Y traits indicates that the expression of these traits is determined by dominance genetic effects. Complementary and duplicate gene actions may account for the superiority of these crosses (Griffings 1956; Baker 1978; Girase and Deshmukh 2000). Therefore, these hybrids are expected to produce desirable segregants and could be exploited successfully in pea varietal improvement programs. GCA variance was lower than SCA for all characters except DF. The ratio of GCA variance to SCA variance (Baker index) was much lower than 1, ranging from 0.00 to 0.44 for NP (Table 1) for all characters studied. This indicates the predominant role of non-additive gene actions in the inheritance of all those traits in pea. Sharma et al., (1999) and Malarvizhi (2000) reported the importance of non-additive gene actions for pod yield and pods per plant. Ceyhan (2003) demonstrated that seed yield, pods per plant, seeds per plant, pod yield and 100 seed weight are controlled by non-additive genes. Borah (2009) showed that variance due to general combining ability (GCA) and variance due to specific combining ability (SCA) were highly significant for days to maturity, plant height, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant, while they were non-significant for number of branches per plant, pod length and protein content, indicating the importance of both the additive and non-additive genetic components of variance for these characters. An important influence of non-additive gene action on seed yield in pea has been frequently reported in the literature (Singh and Singh, 1990; Kumar et al., 1996).

**Table 1.** Studied pea accessions.

| Cultivars | Origins |
|---|---|
| CAN A | Canada |
| KEOMA | Canada |
| EXLORER | Canada |
| EI | Canada |
| DDR11 | India |
| DMR7 | India |
| DDR14 | India |
| COME | France |
| C2001 | Local Breeding Program |
| ZAV10 | Local Breeding Program |
| ZAV26 | Local Breeding Program |
| ZAV5 | Local Breeding Program |
| ZAV20 | Local Breeding Program |
| ZAV23 | Local Breeding Program |
| ZAV17 | Local Breeding Program |
| ZAV25 | Local Breeding Program |
| ZAV12 | Local Breeding Program |
| ZAV15 | Local Breeding Program |
| AMA | Local Breeding Program |
| APA | Local Breeding Program |
| MARINA | Romania |
| VIPER | Holland |
| TURF | Russia |

***Estimates of genetic components***

The ratio of additive variance to phenotypic variance (narrow-sense heritability) expresses the extent to which phenotypes are determined by the genes transmitted by the parents. The ratio also expresses the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of a population through selection (Dabholkar, 1992; Holland et al., 2003). Estimates of narrow-sense heritability showed that highest value was 0.65 for DF, suggesting that selection for this trait would be more efficient than that for other traits. Similar results were found by Espinosa and Ligarreto 2005). Estimates of broad-sense heritability showed that the highest value was 0.93 for NS (Table 1). This high value indicates that the trait is highly heritable, and that no environmental agent is being responsible for its phenotypic manifestation (Dabholkar, 1992, Dudley and Moll, 1969). If heritability of a character is very high, for example, 0.8 or more, selection for the character should be fairly easy (Singh and Singh, 2005). This is because there would be a close correspondence between the genotype and the phenotype due to a relatively smaller contribution of the environment to the phenotype.

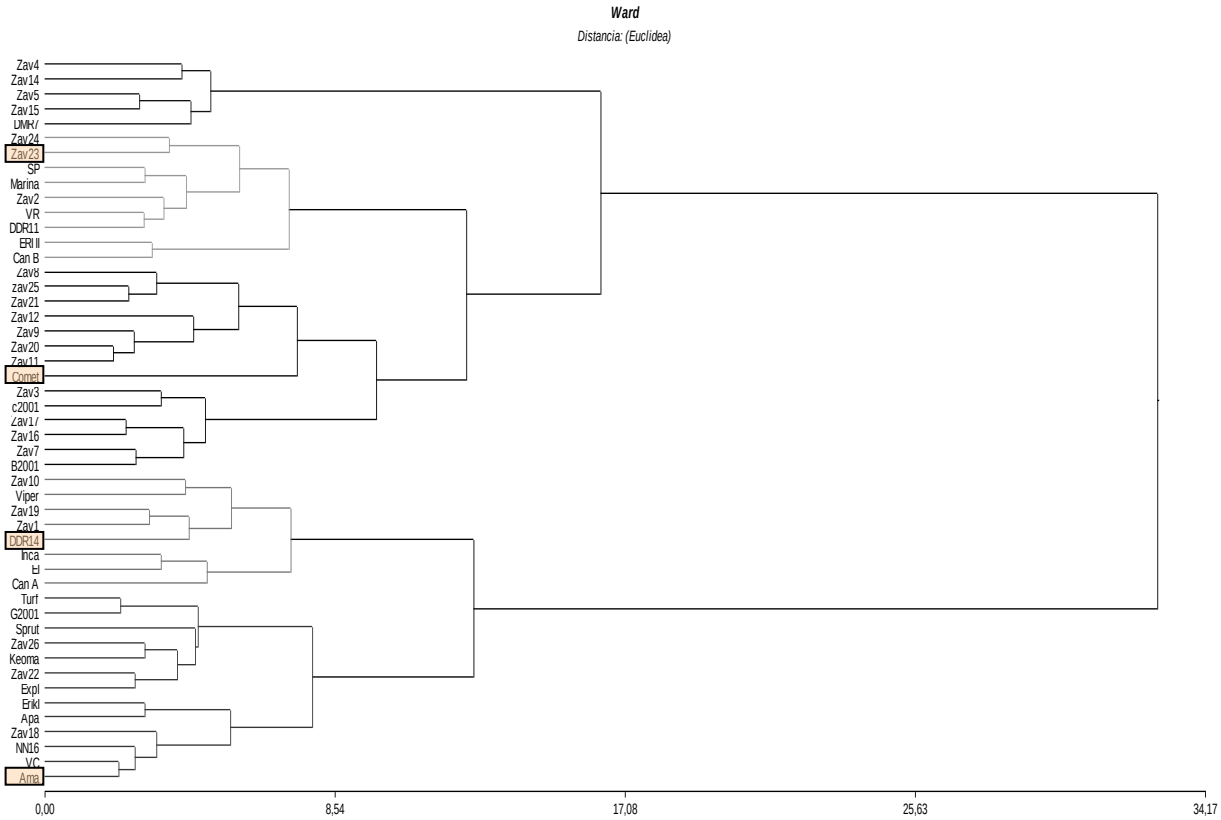


**Fig 1.** Dendrogram of 49 accessions based on morphological data using Euclidean distance matrix. Mean values for each morphological trait in the different clusters are as follows:

| | Group 1 | Group 2 | Group 3 | Group 4 | Group 5 |
|---|---|---|---|---|---|
| Y | 508,2[a] | 798,42[c] | 710,41[b] | 714,84[b] | 427,84[a] |
| NP | 607,22[a] | 1082,22[c] | 722,03[a] | 874,79[b] | 605,66[a] |
| NS | 2609,28[a] | 3566,9[b] | 3190,63[b] | 4184,23[c] | 2549,88[a] |
| FD | 89,22[b] | 95,46[c] | 83,66[a] | 92,21[b] | 84,49[a] |

The values followed by the same letter are not different at the 5% level.

A high heritability implies that the genetic variation for a trait can be precisely assessed from phenotypic observations (broad-sense) and that the trait can be easily transmitted to the offspring of the selected genotypes (narrow sense) (Sharma et al., 2003; Sharma et al., 2007).

***Heterosis and heterotic group***

A large number of hybrids showed superiority over their parents for various traits, indicating the existence of substantial heterosis in the hybrids (Table 3) and the potential of these hybrids for further inbred lines development. BPH of the 76 hybrids varied from -61.0% ('ZAV17 x DDR14') to 274.3% ('DMR7 x COME'). Based on yield-specific combining ability data (SCA), the varieties were classified into four heterotic groups (Table 4). Positive values for SCA between inbred lines generally indicate that the lines are in different heterotic groups (Vasal et al., 1992), while negative SCA values indicate that the lines are in the same heterotic group. Heterotic grouping is a tool for sorting, managing and sampling germplasm without which breeding programs might rely on crossing and testing parents in a more haphazard manner. Our experiment showed that in general, yield, heterosis and specific combining ability (SCA) are higher in inter-groups crosses than in intra-group crosses (Fig 2). This is consistent with theoretical expectations that SCA and heterosis would be lower in crosses within a heterotic group than in crosses between groups. No information about heterotic groups in pea has been published to date. This is the first attempt to group varieties of peas into heterotic groups in order to facilitate the selection of materials to hybridize for new commercial varieties. Information from the genetic diversity of the genotypes is useful for the formation of heterotic populations for the development of varieties in breeding programs. The genotypes used in this study, in general, were found to be useful sources of genetic variability for the development of new genotypes.

**Materials and methods**

***Breeding material and field procedure***

During 2010-2011, 76 hybrids and 23 parents were evaluated at the Experimental Field of the College of Agricultural Sciences, Rosario National University, located in Zavalla (33° 1´ S and 60° 53´ W). Four male lines (of different genetic stocks) and 19 female lines were used for the crosses (Table 1). The pea collection had been previously assessed during two seasons (2008 and 2009), and the morphological traits were subjected to cluster analysis to select the

**Table 2.** ANOVA procedure for numbers of pods (NP), yield (g per plot), numbers of seeds per plot (NS), weigh 100 seed (WS) and numbers of days to flowering (DF).

| | Df | NP | Y | NS | WS | DF |
|---|---|---|---|---|---|---|
| TREATMENTS | 98 | 531385.46 | 400667.85** | 8310580.32** | 286.90** | 19.34** |
| PARENTS | 22 | 154646.97ns | 105276.08** | 2200761.55** | 68.57** | 24.40** |
| LINES | 18 | 175883.03ns | 104792.78** | 2326991.78** | 42.49** | 25.57** |
| TESTER | 3 | 22343.49ns | 77599.26** | 2110084.49** | 133.91** | 6.44ns |
| LINE X TESTER | 1 | 169308.29ns | 197005.96** | 200648.72** | 341.98** | 57.28** |
| PARENTS VS CROSSES | 1 | 12742530.47** | 8922240.18** | 186109699.81** | 336.42** | 264.09** |
| CROSSES | 75 | 479080.15 | 373695.14** | 7732138.90** | 350.29** | 14.59** |
| GCA LINES | 18 | 464869.05ns | 409217.37ns | 10244632.92** | 417.48 | 33.13** |
| GAC TESTERS | 3 | 888512.11** | 117203.62ns | 14479838.87** | 403.09 | 58.01** |
| SCA LINE X TESTER | 54 | 461070.96 | 376103.92** | 6519768.67** | 324.95** | 6.00ns |
| ERROR | 99 | 408326 | 5898 | 56491 | 14 | 6 |
| √ACG | | 2.50 | 5235.23 | 0.00 | 352433.21 | 7.36 |
| √ACE | | 0.00 | 26372.48 | 185102.96 | 3231638.84 | 155.48 |
| BAKER INDEX | | 0.00 | 0.44 | 0.00 | 0.30 | 0.16 |
| $h^2$ | | 0.65 | 0.00 | 0.00 | 0.18 | 0.09 |
| $H^2$ | | 0.65 | 0.00 | 0.88 | 0.93 | 0.77 |

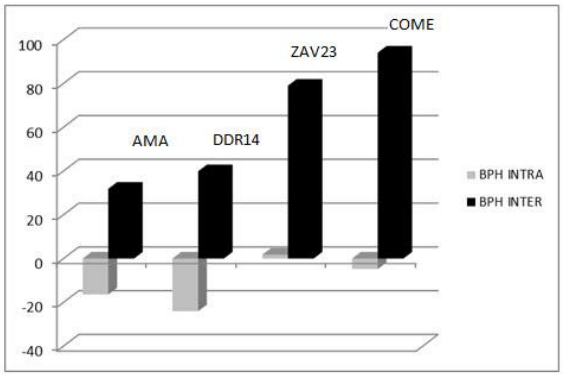


**Fig 2.** Percentaje of intra-goup and inter-group heterosis for each tester.

**Table 3.** General combining ability (GCA) of 23 accessions of pea.

| LINES | NP | Y | NS | DF | WS |
|---|---|---|---|---|---|
| VIP | 66.97 | -46.05 | -215.97 | 4.12 | -3.46 |
| CAN A | 231.89 | 185.23 | 632.08 | -1.95 | 9.55 |
| ZAV12 | -106.24 | 205.41 | -520.63 | 0.74 | 4.62 |
| C2001 | 217.45 | 141.36 | 2434.45 | 0.80 | -6.67 |
| ZAV20 | -246.74 | 366.03 | -1040.51 | 1.30 | 13.70 |
| EI | 198.76 | 29.84 | 1411.43 | 0.99 | -7.45 |
| APA | -143.63 | -63.15 | 269.89 | -0.07 | -5.75 |
| EXPL | 89.83 | 287.74 | -112.24 | 0.18 | 3.69 |
| KEO | -250.36 | 18.47 | -980.01 | 0.62 | 17.50 |
| ZAV10 | -259.96 | -370.03 | -1063.07 | -1.57 | 0.82 |
| DMR7 | -1.42 | 56.33 | -548.88 | 0.99 | 3.93 |
| ZAV25 | 535.18 | 13.49 | 1198.33 | -3.88 | -6.50 |
| ZAV17 | -216.82 | -243.70 | -1465.63 | -0.20 | 2.23 |
| ZAV15 | -229.99 | -286.02 | 41.24 | 1.99 | -8.93 |
| TURF | -352.28 | -391.26 | -2155.17 | -1.01 | 2.01 |
| ZAV5 | -138.74 | 86.14 | -256.67 | 3.43 | 0.60 |
| MAR | 309.18 | 246.33 | 1260.41 | -2.20 | -5.05 |
| DDR11 | 133.56 | -304.61 | 135.74 | -1.76 | -7.42 |
| ZAV26 | 163.35 | 68.42 | 975.20 | -2.51 | -7.40 |
| TESTERS | | | | | |
| AMA | -116.65 | -50.94 | -391.94 | 0.73 | -1.45 |
| DDR14 | 71.84 | -12.19 | 538.28 | 1.25 | -4.68 |
| ZAV23 | 181.11 | 79.08 | 513.81 | -1.50 | 0.88 |
| COME | -136.29 | -15.96 | -660.15 | -0.48 | 5.25 |

**Table 4.** Specific combining ability (SCA) of 76 hybrids.

| HYBRIDS | NP | Y | NS | DF | WS |
|---|---|---|---|---|---|
| VIPXAMA | -558.93 | 18.66 | -965.85 | -0.23 | 8.11 |
| VIPXDDR14 | 215.58 | 431.01 | 1398.43 | -2.50 | -1.42 |
| VIPXZAV23 | -281.19 | -292.68 | -927.43 | 2.00 | -0.49 |
| VIPXCOME | 624.54 | -156.98 | 494.86 | 0.73 | -6.20 |
| CAN AXAMA | -283.35 | -117.27 | -926.39 | -0.67 | -11.86 |
| CAN AXDDR14 | 205.66 | -335.45 | 605.05 | -0.68 | -14.50 |
| CAN AXZAV23 | -91.95 | 71.16 | 192.02 | -0.43 | 35.28 |
| CAN AXCOME | 169.63 | 381.56 | 129.32 | 1.79 | -8.92 |
| ZAV12XAMA | -82.72 | 254.80 | 118.82 | -0.86 | 14.26 |
| ZAV12XDDR14 | 91.29 | 399.05 | 991.09 | 0.13 | 1.69 |
| ZAV12XZAV23 | 502.01 | -55.73 | -194.43 | 2.13 | -6.48 |
| ZAV12XCOME | -510.58 | -598.12 | -915.48 | -1.40 | -9.47 |
| C2001XAMA | 948.10 | 95.88 | 3145.61 | -0.17 | -0.43 |
| C2001XDDR14 | 227.10 | 370.94 | 268.34 | 0.57 | 3.44 |
| C2001XZAV23 | -723.97 | -277.67 | -845.63 | 0.32 | -2.42 |
| C2001XCOME | -451.23 | -189.15 | -2568.33 | -0.71 | -0.59 |
| ZAV20XAMA | -535.22 | -651.87 | -680.81 | 0.83 | -17.66 |
| ZAV20XDDR14 | -378.21 | -388.77 | -571.53 | -0.18 | -5.10 |
| ZAV20XZAV23 | 860.01 | 623.40 | 1532.94 | -0.68 | 3.95 |
| ZAV20XCOME | 53.42 | 417.24 | -280.60 | 0.04 | 18.82 |
| EIXAMA | 42.28 | -385.53 | -868.24 | 0.60 | -2.60 |
| EIXDDR14 | 558.79 | 418.41 | 1649.03 | 0.13 | 4.99 |
| EIXZAV23 | -477.99 | -427.91 | -2471.50 | 2.63 | 1.26 |
| EIXCOME | -123.08 | 395.03 | 1690.71 | -3.15 | -3.66 |
| APAXAMA | -271.99 | 107.63 | -1531.70 | -0.80 | 11.08 |
| APAXDDR14 | -222.57 | -97.44 | -978.59 | 1.19 | 0.93 |
| APAXZAV23 | 105.24 | -243.81 | 1027.55 | 0.19 | -7.86 |
| APAXCOME | 389.31 | 233.63 | 1482.75 | -0.59 | -4.16 |
| EXPLXAMA | -396.28 | 306.72 | -1749.58 | 0.95 | 20.71 |
| EXPLXDDR14 | -271.03 | -358.64 | -356.05 | -2.31 | -2.43 |
| EXPLXZAV23 | 677.95 | 369.19 | 1533.67 | 0.19 | -4.17 |
| EXPLXCOME | -10.64 | -317.27 | 571.96 | 1.16 | -14.11 |
| KEOXAMA | -313.60 | -406.76 | -1041.81 | 4.27 | -16.10 |
| KEOXDDR14 | 1042.91 | 399.81 | 3507.47 | -2.75 | -19.39 |
| KEOXZAV23 | -613.03 | -250.04 | -1113.72 | -0.75 | -14.63 |
| KEOXCOME | -116.29 | 256.99 | -1351.94 | -0.77 | 50.12 |
| ZAV10XAMA | -308.16 | 22.58 | -1493.74 | 0.45 | 8.46 |
| ZAV10XDDR14 | 5.37 | -319.26 | -215.40 | -0.06 | -2.64 |
| ZAV10XZAV23 | 1.15 | 594.09 | 1095.51 | -1.81 | 12.43 |
| ZAV10XCOME | 301.64 | -297.41 | 613.63 | 1.41 | -18.24 |
| DMR7XAMA | 48.72 | -359.62 | 733.32 | -0.36 | -15.72 |
| DMR7XDDR14 | 256.47 | 343.88 | 979.34 | 1.13 | 3.37 |
| DMR7XZAV23 | -434.80 | -747.40 | -3455.43 | -0.62 | 0.85 |
| DMR7XCOME | 129.61 | 763.14 | 1742.77 | -0.15 | 11.50 |
| ZAV25XAMA | -197.64 | -111.73 | -1295.14 | 0.02 | 1.31 |
| ZAV25XDDR14 | 586.12 | 324.96 | 1045.88 | 0.25 | 3.91 |
| ZAV25XZAV23 | 132.68 | 14.89 | 2140.36 | 0.00 | -0.30 |
| ZAV25XCOME | -521.16 | -228.12 | -1891.10 | -0.27 | -4.92 |
| ZAV17XAMA | 361.36 | 182.81 | 950.48 | -0.67 | -5.23 |
| ZAV17XDDR14 | -430.63 | -501.84 | -3511.41 | 5.57 | 6.89 |
| ZAV17XZAV23 | 324.26 | 113.62 | 1728.90 | -3.68 | -9.88 |
| ZAV17XCOME | -255.00 | 205.42 | 832.02 | -1.21 | 8.22 |
| ZAV15XAMA | 706.03 | 593.48 | 2994.44 | -1.86 | 2.63 |
| ZAV15XDDR14 | -507.46 | -65.32 | -2168.28 | -0.37 | 9.50 |
| ZAV15XZAV23 | -89.24 | -360.55 | -551.31 | 0.13 | -7.26 |
| ZAV15XCOME | -109.33 | -167.61 | -274.85 | 2.10 | -4.87 |
| TURFXAMA | 270.82 | 280.07 | 175.86 | -1.36 | 5.68 |
| TURFXDDR14 | 189.83 | -46.78 | -166.87 | 0.13 | -3.67 |

| | | | | | |
|---|---|---|---|---|---|
| TURFXZAV23 | -233.61 | 62.61 | 1158.44 | 1.13 | -10.20 |
| TURFXCOME | -227.04 | -295.89 | -1167.44 | 0.10 | 8.19 |
| ZAV5XAMA | -7.72 | -435.78 | 1047.36 | 0.95 | -9.34 |
| ZAV5XDDR14 | 6.29 | -3.33 | -505.37 | -1.06 | 4.64 |
| ZAV5XZAV23 | 227.01 | 824.44 | 748.27 | -1.31 | 7.58 |
| ZAV5XCOME | -225.58 | -385.33 | -1290.27 | 1.41 | -2.88 |
| MARXAMA | 767.28 | 701.39 | 1924.44 | -0.92 | 3.53 |
| MARXDDR14 | -565.38 | -668.20 | -1062.45 | 1.07 | -1.12 |
| MARXZAV23 | -130.90 | 232.68 | -1032.97 | -0.18 | 7.55 |
| MARXCOME | -71.00 | -265.87 | 170.98 | 0.04 | -9.96 |
| DDR11XAMA | -96.68 | 46.59 | -907.56 | 0.89 | 3.54 |
| DDR11XDDR14 | -490.17 | -146.36 | -709.78 | -1.87 | 5.63 |
| DDR11XZAV23 | 398.89 | 278.70 | 2815.03 | 0.13 | -4.74 |
| DDR11XCOME | 187.96 | -178.93 | -1197.69 | 0.85 | -4.43 |
| ZAV26XAMA | -92.30 | -142.01 | 370.48 | -0.86 | -0.37 |
| ZAV26XDDR14 | -519.96 | 243.35 | -198.91 | 1.63 | 5.28 |
| ZAV26XZAV23 | -152.57 | -528.99 | -3380.27 | 0.63 | -0.45 |
| ZAV26XCOME | 764.83 | 427.65 | 3208.69 | -1.40 | -4.46 |

**Table 5.** Estimate of Best Parent Heterosis (BPH).

| Hybrids | BPH (%) |
|---|---|
| APAXAMA | 27.7 |
| APAXCOME | 49.1 |
| APAXDDR14 | -0.5 |
| APAXZAV23 | 4.8 |
| C2001XAMA | 49.5 |
| C2001XCOME | 41.3 |
| C2001XDDR14 | 69.2 |
| C2001XZAV23 | 42.2 |
| CAN AXAMA | 20.2 |
| CAN AXCOME | 75.9 |
| CAN AXDDR14 | 0.6 |
| CAN AXZAV23 | 53.4 |
| DDR11XAMA | -6.6 |
| DDR11XCOME | 20.1 |
| DDR11XDDR14 | -30.5 |
| DDR11XZAV23 | 62.7 |
| DMR7XAMA | -11.7 |
| DMR7XCOME | 274.3 |
| DMR7XDDR14 | 57.6 |
| DMR7XZAV23 | -28.4 |
| EIXAMA | -17.6 |
| EIXCOME | 198.1 |
| EIXDDR14 | 62.6 |
| EIXZAV23 | 11.7 |
| EXPLXAMA | 90 |
| EXPLXCOME | 94.7 |
| EXPLXDDR14 | 8.8 |
| EXPLXZAV23 | 156.3 |
| KEOXAMA | -21.3 |
| KEOXCOME | 141.8 |
| KEOXDDR14 | 59.5 |
| KEOXZAV23 | 35.4 |
| MARXAMA | 130 |
| MARXCOME | 45.7 |
| MARXDDR14 | -30.6 |
| MARXZAV23 | 124.4 |
| TURFXAMA | 10.1 |
| TURFXCOME | -16.7 |
| TURFXDDR14 | -22.6 |
| TURFXZAV23 | 21.2 |
| VIPXAMA | 19.6 |
| VIPXCOME | 36.6 |
| VIPXDDR14 | 56 |
| VIPXZAV23 | 19.9 |
| ZAV10XAMA | -16.7 |
| ZAV10XCOME | -44.6 |
| ZAV10XDDR14 | -55.2 |
| ZAV10XZAV23 | 76.6 |
| ZAV12XAMA | 74.8 |
| ZAV12XCOME | 6.9 |
| ZAV12XDDR14 | 78.3 |
| ZAV12XZAV23 | 86.8 |
| ZAV15XAMA | 57.5 |
| ZAV15XCOME | 28.4 |
| ZAV15XDDR14 | -20.2 |
| ZAV15XZAV23 | -22.5 |
| ZAV17XAMA | 15.8 |
| ZAV17XCOME | 108.6 |
| ZAV17XDDR14 | -61 |
| ZAV17XZAV23 | 48.5 |
| ZAV20XAMA | -9.7 |
| ZAV20XCOME | 267.3 |
| ZAV20XDDR14 | 13.8 |
| ZAV20XZAV23 | 202 |
| ZAV25XAMA | 4.1 |
| ZAV25XCOME | -4.5 |
| ZAV25XDDR14 | 51.2 |
| ZAV25XZAV23 | 31.2 |
| ZAV26XAMA | 14.3 |
| ZAV26XCOME | 109.3 |
| ZAV26XDDR14 | 48.4 |
| ZAV26XZAV23 | -2.4 |
| ZAV5XAMA | -16.9 |
| ZAV5XCOME | 58.2 |
| ZAV5XDDR14 | 24.7 |
| ZAV5XZAV23 | 191.1 |

**Table 6.** Heterotic groups based on yield-specific combining ability data (SCA).

| AMA | DDR14 | ZAV23 | COME |
|---|---|---|---|
| ZAV20 | CANA | VIPER | ZAV12 |
| EI | APA | C2001 | ZAV25 |
| KEOMA | EXPLORER | DMR7 | TURF |
| ZAV5 | ZAV10 | ZAV15 | |
| | ZAV17 | ZAV26 | |
| | MARINA | | |
| | DDR11 | | |

appropriate testers (Fig. 1). The hybrids along with parent lines were grown in a randomized block design with two replications. Each plot consisted of one 3-m long row with spacing of 10 cm between plants.

***Traits measurements and statistical analysis***

Data for five traits were collected: Number of days to flowering (DF), number of pods (NP), number of seeds per plot (NS), yield (in g per plot) (Y) and weight of 100 seed (WS) measured at the dry seed stage.
Data were analyzed with ANOVA, and the combining ability analysis was carried out as suggested by Kempthorne (1957). Statistical analyses were calculated with GENES software (Cruz, 2006).
Heterosis for hybrids yield was calculated with the formula proposed by Kempthorne (1957):

$$BPH = \left(\frac{F1-BP}{BP}\right) * 100$$

Where $F_1$ is the mean of the $F_1$ hybrid performance and HP = the best parental performance. Specific combining ability

(SCA) effects were estimated for yield according to established methods (Hallauer and Miranda, 1988).
The GCA:SCA ratios, with a theoretical maximum of 1 for each trait, were calculated according to Baker (1978) as follows:

$$GCA/_{SCA} = \frac{2\sigma 2gi}{(2\,\sigma 2gi + \sigma 2sij)}$$

Where gi = the GCA effect of the *i* parent and sij = the SCA effect of the cross *i x j*.
Values of narrow and broad sense heritability were calculated for each trait using Falconer's methods (Falconer and Mackay, 1996).

**Conclusions**

Knowledge of the relative heritability of the various traits can aid in the design of efficient breeding systems where many traits need to be improved simultaneously (Jones, 1986). Heterotic groups were formed on the basis of the SCA values for yield. The proposed heterotic groups were confirmed by comparing intra and inter-groups $F_1$ values and best-parent heterosis. According to our results, selection of best cross combinations should be based on GCA and SCA values. The heterotic crosses obtained in this study can be easily exploited in segregating generations to develop high-yielding varieties. The identification of heterotic groups among breeding lines provides fundamental information to plant breeders. These heterotic groups must be confirmed by estimating the genetic distance between parental lines through molecular markers to predict heterosis to simplify the screening of parents.

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