Grouping sunflower genotypes by reaction to alternaria leaf spot (*Alternaria helianthi*) and yield

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ABSTRACT

- The objective of this paper was to group sunflower genotypes based on the reaction to Alternaria leaf spot disease, yield and 1000-seed weight, using the multivariate method of Principal Component Analysis (PCA).
- Forty-nine sunflower genotypes were evaluated on field experiments, in Londrina, state of Parana, Brazil, during 2003/2004, 2004/2005, 2005/2006, 2007/2008 e 2008/2009 growing seasons. Alternaria disease severity, under natural conditions in the field, was evaluated at the R3 growth stage with reference to a diagrammatic scale developed for this disease. After harvesting, yield (kg ha^{-1}) and 1000-seed weight (g) were also evaluated.
- The method of PCA was useful for grouping sunflower genotypes as a function of the studied variables.
- Genotypes with desirable agronomic characteristics (high yield and high resistance or tolerance to disease) are placed in the first quadrant. Less productive sunflowers are located in the third quadrant.
- Since no complete resistance to Alternaria leaf spot has been observed yet on sunflower genotypes, efforts to obtain cultivars with higher level of resistance should be continued.

Key words: Alternaria leaf spot – disease resistance - *Helianthus annuus* – principal component analysis

INTRODUCTION

Alternaria leaf spot caused by *Alternaria helianthi* has been prevalent in sunflower crop in Brazil, occurring in virtually all regions and sowing dates. The damage caused by the disease can be due to the reduction of plant photosynthetic area, formation of leaf spots and early defoliation, resulting in reduced achene diameter, number of achenes per chapter, weight of 1000 seeds and oil content (Davet et al., 1991; Leite, 2005).

Effective disease control is very difficult when epidemic is already occurring in the field. Among the strategies for managing the disease, genetic resistance is highly desirable because it is the most economical way to reduce the damage caused by the pathogen (Davet et al., 1991). Information about the reaction of hybrids and cross-pollinated varieties to Alternaria leaf spot is available in other countries and some information has been generated recently in Brazil (Leite et al., 1999; Leite and Carvalho, 2005; Leite et al., 2007; Leite and Oliveira, 2009). Since this is a work in progress, it is interesting to compare the results obtained in different crop seasons, considering that these experiments have a common standard genotype (M 734), evaluated in all seasons.

Whereas the results obtained in different years are of different genotypes, it is not possible to perform analysis of variance (ANOVA) combined with only one common genotype. The most appropriate method to group sunflower genotypes as a function of the evaluated variables is the multivariate method of Principal Component Analysis (PCA), which allows the sorting or grouping without losing information. In addition, it linearly transforms a large number of variables into a non-correlated smaller set of them (Silva and Padovani, 2006).

The objective of this paper was to group sunflower genotypes based on the reaction to Alternaria leaf spot disease, yield and 1000-seed weight, using the multivariate method of Principal Component Analysis.

MATERIAL AND METHODS

Forty-nine sunflower genotypes were evaluated for resistance to Alternaria leaf spot under field conditions in the experimental area at Embrapa Soja, Londrina, PR, Brazil, during 2003/2004, 2004/2005, 2005/2006, 2007/2008 and 2008/2009 growing seasons. In the first three years, we studied 10 sunflower genotypes and in the last two growing seasons, 12 materials were evaluated. Experimental design was a randomized block design, with 10:12 genotypes and four replications.

In all experiments, a common genotype was included, the sunflower hybrid M734.

The experiments were sown in November 2003, November 2004, November 2005, October 2007 and October 2008. Each plot consisted of 4 rows of 4 m, spaced 0.80 m, with three plants per linear meter. We followed the recommendations for sunflower crop, including fertilization, weed control, spraying against insects and irrigation when necessary. No artificial inoculation of *A. helianthi* was performed, since the disease occurred by natural infection of plants by the fungus. The pathogen was identified through laboratory isolation and inoculation of plants in a greenhouse.

Assessments of disease severity (%) were performed in two central rows of each plot, discarding 0.5 m from each end of the line. The individual plant system was adopted (Kranz and Jörg, 1989), where five homogeneous plants in each plot were marked. The plants were chosen during V4 stage (Schneiter and Miller, 1981), taking care to select individuals of the same development, time and place. Total leaf area was estimated on marked plants (Leite and Amorim, 2002) in the developmental stage R3 (Schneiter and Miller, 1981). Simultaneously, Alternaria disease severity (%) was estimated on all leaves using diagrammatic scale of the disease, previously developed and validated (Leite and Amorim, 2002).

Plants were harvested individually, after physiological maturity stage (R9) (Schneiter and Miller, 1981) and yield (kg ha^{-1}) and 1000-seed weight (g) were evaluated at 11% humidity.

Using the method of Principal Component Analysis, the coefficients of the components were obtained by the eigenvectors of the correlation matrix among measures of the response variables yield (kg ha^{-1}), Alternaria disease severity (%) and 1000-seed weight (g), standardized with distribution $N \cong (0.1)$, so that the three variables were dimensionless after standardization. Analyses were performed using SAS and Statistica programs (Statsoft, 1995, SAS, 2001).

RESULTS AND DISCUSSION

It was possible to group sunflower genotypes depending on the variables yield, Alternaria severity and 1000-seed weight, using the multivariate method of Principal Component Analysis. The eigenvalues obtained for the three components were, respectively, 1.3819, 0.9946 and 0.6234, totalizing 100% of the total variation. Based on these eigenvalues, the results of PCA indicated that the first component accounted with 46.07%, the second with 33.15% and third with 20.78% of the total variation among the variables. For PCA, the number of principal components is always equal to the number of variables considered in the research, but not always the number of components or selected axes is equal to the maximum number of variables. Usually, the first two components explain the whole total variation of a larger number of variables, that the first component is the most important because it has the greatest contribution to the variation of the data (Silva and Padovani, 2006). Thus, the first two principal components or two axes explained 79.99% of the total variation.

The correlation between the variables disease severity and yield was 0.006, yield and 1000-seed weight was 0.2013 and the highest correlation was achieved between severity and 1000-seed weight (0.3215). Observing the first component (46.07%), the coefficients were all positive and the largest contribution in the study was attributed to 1000-seed weight, and secondly, to disease severity. In the second component (33.15%), the largest contribution was from yield, with a positive coefficient, and the others were negative. For the last component with the lowest contribution (20.78%), all coefficients were negative (Table 1).

Table 1. Values of principal components and contribution of the variables yield (kg ha^{-1}), Alternaria leaf spot severity (%) and 1000-seed weight (g).

Variables	Principal component 1	Principal component 2	Principal component 3
Yield (kg ha^{-1})	0,3806	0,8475	-0,3697
Alternaria leaf spot severity (%)	0,5988	-0,5306	-0,5998
1000-seed weight (g)	0,7045	-0,0068	-0,7095

The genotypes of the various groups in the quadrants are related as follows:
Quadrant 1: **G_1** = M734-01**,** Agrobel 967, Agrobel 972, CATI 01, EXP38 and Nutrissol; **G_2** = M734-02, Multissol 08, V10034, MG52, M734-05 and Zenit;
Quadrant 2: **G_3**= Helio 250, Agrobel 962, Agrobel 959 and Guarani; **G_4**= Helio 251, M734-02, Helio 355 and Helio 358; **G_5**= Embrapa 122, BHS02 and EXP1447;
Quadrant 3: **G_6** = BHS03, MG50 and HLE02; **G_7**= BHS05 and BRSGIRA15; **G_8**= BHS04, V 02038, M734-04, V50386 and HLA04; **G_9**= BRSGIRA12, BRSGIRA13, BRSGIRA14, EXP1446, HELIO256 and HLE01;
Quadrant 4: **G_{10}**= V90064 and V80198; **G_{11}**= BHS01, V03005 and BRSGIRA11; **G_{12}**= M734-03, BRSGIRA01, BRSGIRA09, BRSGIRA24, BRSGIRA25, Embrapa 01, HLA863, Neon and Triton; **G_{13}**= Grizzly.

Most productive sunflower genotypes were located in the first quadrant, which was divided into two groups. The first group (G_1) is associated with the highest yields and the lowest severity, ie, greater resistance to disease, such as genotype EXP38 (2785.37 kg ha^{-1}), with higher yield than the standard M734-01 (2442.63 kg ha^{-1}). This first group of genotypes were evaluated in the 2003/2004 season, when the experiment showed very good average yield (2127 kg ha^{-1}) (Leite and Carvalho, 2005). In G_2, the yields were good, ranging from 1263.46 to 1622.58 kg ha^{-1}, despite higher disease severity, indicating disease tolerance of the genotypes. In the second quadrant, yields varied from 715.22 to 1843.60 kg ha^{-1} and it was divided into three groups. The third quadrant grouped the genotypes with the lowest yields (from 436.13 to 1120.23 kg ha^{-1}) and the lowest 1000-seed weight (31.95 to 43.12 g). Despite the relatively low disease severity values (5.27 to 15.77%), the genotypes in the third quadrant showed low yield potential. Of the fifteen hybrids in the fourth quadrant, only four had yields lower than 1000 kg ha^{-1} and the others ranged from 1042.38 to 1571.01 kg ha^{-1}. These yields are higher than those of genotypes in the third quadrant, but they were placed in the fourth quadrant due to disease severity values above 14%. In the group G_{13}, the confectioner sunflower Grizzly stood out for having the largest 1000-seed weight (99.35 g) between the genotypes.

Since no complete resistance to Alternaria leaf spot has been observed on sunflower genotypes evaluated so far, in Brazilian conditions (Leite et al., 1999; Leite and Carvalho, 2005; Leite et al., 2007; Leite and Oliveira, 2009), efforts to obtain cultivars with higher levels of resistance should be continued.

CONCLUSIONS

The method of Principal Component Analysis is useful for grouping sunflower genotypes as a function of Alternaria leaf spot severity, yield and 1000-seed weight. Sunflower genotypes with desirable agronomic characteristics (higher productivity and greater disease resistance or tolerance) are placed in the first quadrant. Less productive sunflowers are located in the third quadrant.

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