Grouping sunflower genotypes for yield, oil content, and reaction to Alternaria leaf spot using GGE biplot

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Abstract – The objective of this work was to evaluate the suitability of the multivariate method of principal component analysis (PCA) using the GGE biplot software for grouping sunflower genotypes for their reaction to Alternaria leaf spot disease (*Alternariaster helianthi*), and for their yield and oil content. Sixty-nine genotypes were evaluated for disease severity in the field, at the R3 growth stage, in seven growing seasons, in Londrina, in the state of Paraná, Brazil, using a diagrammatic scale developed for this disease. Yield and oil content were also evaluated. Data were standardized using the software Statistica, and GGE biplot was used for PCA and graphical display of data. The first two principal components explained 77.9% of the total variation. According to the polygonal biplot using the first two principal components and three response variables, the genotypes were divided into seven sectors. Genotypes located on sectors 1 and 2 showed high yield and high oil content, respectively, and those located on sector 7 showed tolerance to the disease and high yield, despite the high disease severity. The principal component analysis using GGE biplot is an efficient method for grouping sunflower genotypes based on the studied variables.

Index terms: *Alternariaster helianthi*, *Helianthus annuus*, disease resistance, principal component analysis.

Agrupamento de genótipos de girassol quanto à produtividade, ao teor de óleo e à reação à mancha de alternária por GGE biplot

Resumo – O objetivo deste trabalho foi avaliar a adequação do uso do método multivariado de análise de componentes principais (ACP), com uso do programa GGE biplot, para o agrupamento de genótipos de girassol quanto à sua reação à mancha de alternária (*Alternariaster helianthi*), e quanto à produtividade e ao teor de óleo. Sessenta e nove genótipos foram avaliados quanto à severidade da doença em campo, na fase de desenvolvimento R3, em sete safras, em Londrina, PR, com uso de uma escala diagramática própria, desenvolvida para esta doença. A produtividade e o teor de óleo também foram avaliados. Os dados foram padronizados com o programa Statistica, e o GGE biplot foi utilizado para ACP e exibição gráfica dos dados. Os dois primeiros componentes principais explicaram 77,9% da variação total. De acordo com o biplot poligonal, obtido com os dois primeiros componentes principais e as três variáveis resposta, os genótipos foram divididos em sete setores. Os genótipos alocados nos setores 1 e 2 apresentaram alta produtividade e alto teor de óleo, respectivamente, e os agrupados no setor 7 apresentaram tolerância à doença e alta produtividade, apesar de elevada severidade da doença. O método de análise de componentes principais com uso do GGE biplot é eficiente para agrupar genótipos de girassol com base nas variáveis estudadas.

Termos para indexação: *Alternariaster helianthi*, *Helianthus annuus*, resistência a doenças, análise de componentes principais.

Introduction

Sunflower (*Helianthus annuus* L.) cropped area is increasing in Brazil, with 144 thousand hectares in the last growing season (Companhia Nacional de Abastecimento, 2014). However, there is an enormous potential for expansion, since sunflower is planted as a second summer crop in succession to soybean, which occupies an area of around 30 million hectares in Brazil (Companhia Nacional de Abastecimento, 2014). The potential for area expansion is also driven by a crescent demand for special oils for human consumption, as high oleic oil, and by the Brazilian government demand for biofuel.

Alternaria leaf spot, caused by *Alternariaster helianthi* (Hansf.) E.G. Simmons (syn. *Alternaria helianthi* (Hansf.) Tubaki & Nishihara), can be a threat for sunflower production in Brazil, since it has been

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prevalent on the crop, occurring in virtually all regions of the country and on all sowing dates. Damage caused by the disease can be due to the reduction of plant photosynthetic area, formation of leaf spots, and early defoliation, which results in the reduction of achene diameter, number of achenes per head, 1000-seed weight, and oil content (Leite et al., 2006; Alves et al., 2013).

An efficient 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 does not add costs to farmers, and sometimes it can remove the need for other control methods (Leite et al., 2006). Although regional crop variety trials for an important crop are conducted every year, the tested genotypes vary from year to year, leading to high unbalanced data across the years. Strategies have been developed to deal with this data (Yan, 2014). It is interesting to compare the results obtained in different crop seasons, considering that these trials have a common standard genotype (Dow M734), evaluated in all years.

As the results of different genotypes are obtained in different years, it is not possible to perform the analysis of variance combined with only one common genotype. In this case, 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 noncorrelated smaller set of them (Silva & Padovani, 2006). Comparing to the univariate method, using a massive array of data, it can interpret a research with few components using the information of all variables (Rao, 1964).

Using PCA to summarize a large number of variables in ecological studies, Prado et al. (2002) measured the importance of each of these variables on each axis or component by its weight, which is correlated with the axis. Such components are measured in linear functions that allow knowing the size and shape of the data variation.

Principal component analysis proposed by Yan & Rajcan (2002), using the software GGE biplot, enables a singular value decomposition (SVD) of the first two principal components, which means that a matrix is decomposed in three parts: singular values, eigenvectors of columns, and eigenvectors of rows, forming a diagonal matrix. Biplot analysis was first developed by Gabriel (1971), and it can interpret multiple variables in function of different treatments in the same graphic (Akinwale et al., 2014). GGE biplot has been used to show the performance of sunflower hybrids in different testing environments or sowing dates (Ullah et al., 2007; Balalic et al., 2012; Brankovic et al., 2012). A GGE biplot is used to analyze multi-year data of variety trials, where genotypes vary from year to year, treating each year-location as an environment (Yan, 2014).

The objective of this work was to evaluate the suitability of the multivariate method of principal component analysis, using the software GGE biplot, for grouping sunflower genotypes for their reaction to Alternaria leaf spot disease (*Alternariaster helianthi*), and for their yield and oil content.

Materials and Methods

For the present experiment, sixty-nine sunflower genotypes were evaluated for their reaction to Alternaria leaf spot under field conditions, in the experimental area of Embrapa Soja, Londrina, PR, Brazil (23°11'37"S, 51°11'03"W, 630 m altitude), in 2002/2003, 2004/2005, 2005/2006, 2007/2008, 2009/2010, 2011/2012 and 2012/2013 growing seasons. In the first three growing seasons, 10 sunflower genotypes were studied, and in the last four growing seasons, 12 genotypes were evaluated (Table 1). The experiment was carried out in a randomized block design, with 10:12 genotypes and four replicates. A common genotype, the sunflower hybrid named Dow M734, was included in all trials. Some genotypes were evaluated twice: the sunflower open-pollinated variety Embrapa 122, in 2002/2003 and 2004/2005, the hybrid Helio 358 in 2004/2005 and 2012/2013, and BRS Gira 30 in 2011/2012 and 2012/2013 growing seasons. Accumulated precipitation for each season is presented in Figure 1.

The trials were sown in November (2002, 2004, and 2005), and in October (2007, 2008, 2009, 2011, and 2012). Each plot consisted of four 4-meter rows spaced at 0.80 m, with three plants per linear meter. The recommendations for sunflower cultivation were followed, 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 on plants in a greenhouse.

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

Table 1. Sunflower genotypes evaluated for grain yield, oil content, and reaction to Alternaria leaf spot in seven growing seasons.

Code	Growing season	Genotype	Code	Growing season	Genotype
A1	2002/2003	Dow M734	D10	2007/2008	HLA 04 (HLA 86)
A2	2002/2003	Agrobel 920	D11	2007/2008	HLE 01
A3	2002/2003	Agrobel 960	D12	2007/2008	HLE 02
A4	2002/2003	BRS 191	E1	2009/2010	Dow M734
A5	2002/2003	Agrobel 965	E2	2009/2010	BRHS 01
A6	2002/2003	C 11	E3	2009/2010	BRS Gira 23
A7	2002/2003	HT 9	E4	2009/2010	BRS Gira 24
A8	2002/2003	Agrobel 910	E5	2009/2010	BRS Gira 26
A9	2002/2003	Morgan M 742	E6	2009/2010	BRS Gira 27
A10	2002/2003	Embrapa 122	E7	2009/2010	NTO 3.0
B1	2004/2005	Dow M734	E8	2009/2010	SRM822
B2	2004/2005	Embrapa 122	E9	2009/2010	V20041
B3	2004/2005	Agrobel 959	E10	2009/2010	EXP 1450 HO
B4	2004/2005	Guarani	E11	2009/2010	HLE 15
B5	2004/2005	Helio 355	E12	2009/2010	HLS 07
B6	2004/2005	Helio 358	F1	2011/2012	Dow M734
B7	2004/2005	Multissol 08	F2	2011/2012	BRS Gira 28
B8	2004/2005	V 90064	F3	2011/2012	BRS Gira 29
B9	2004/2005	V10034	F4	2011/2012	BRS Gira 30
B10	2004/2005	V80198	F5	2011/2012	BRS Gira 31
C1	2005/2006	Dow M734	F6	2011/2012	BRS Gira 32
C2	2005/2006	BHS 01	F7	2011/2012	BRS Gira 33
C3	2005/2006	BHS 02	F8	2011/2012	HLA 44-49
C4	2005/2006	BHS 03	F9	2011/2012	QC 6730
C5	2005/2006	BHS 04	F10	2011/2012	Sulfosol
C6	2005/2006	BHS 05	F11	2011/2012	SYN 039A
C7	2005/2006	V 03005	F12	2011/2012	SYN 042
C8	2005/2006	V 20038	G1	2012/2013	Dow M734
C9	2005/2006	Dow MG 52	G2	2012/2013	BRS 321
C10	2005/2006	Dow MG 50	G3	2012/2013	BRS 322
D1	2007/2008	Dow M734	G4	2012/2013	BRS 323
D2	2007/2008	BRS Gira 12	G5	2012/2013	BRS 324
D3	2007/2008	BRS Gira 13	G6	2012/2013	BRS Gira 26
D4	2007/2008	BRS Gira 14	G7	2012/2013	BRS Gira 30
D5	2007/2008	BRS Gira 15	G8	2012/2013	BRS Gira 34
D6	2007/2008	Exp 1446	G9	2012/2013	BRS Gira 35
D7	2007/2008	Exp 1447	G10	2012/2013	BRS Gira 36
D8	2007/2008	V 50386	G11	2012/2013	BRS Gira 42
D9	2007/2008	Helio 256	G12	2012/2013	Helio 358

simultaneously at R3 growth stage, as recommended by Leite et al. (2006).

Plants were harvested individually, after physiological maturity stage (R9) (Schneiter & Miller, 1981), and yield (kg ha^{-1}) was evaluated at 11% humidity. Oil content (%) was predicted by NIR spectroscopy (Grunvald et al., 2014).

Precipitation was measured during the seven growing seasons (Figure 1), since water deficiency could affect sunflower production and disease development. As data were obtained in different years, original data of the variables were standardized within each growing season, in order to minimize the effect of the environment, and to reduce experimental variability. This procedure was performed using the software Statistica (Statsoft, 1995), after the normalization of the variables – yield (kg ha^{-1}), Alternaria disease severity (%), and oil content (%) – to the same scale as a normal distribution with mean zero and standard deviation one [(N ≅ (0,1)], ensuring that they are dimensionless. Pearson correlation coefficients for original data were assessed by t test, at 5% probability.

Principal component analysis and biplot graphics were performed by data matrix of sunflower genotypes and by singular value decomposition (SVD) focusing on the treatments (interaction between genotype and year). Eigenvalues and eigenvectors of PCA were calculated for yield, Alternaria leaf spot severity, and oil content, using GGE biplot (Yan & Kang, 2003; Yan et al., 2015).

Afterwards, the resulting first two principal components (PC1 and PC2) were taken to perform the biplot analysis and graphical display of data, using the GGE biplot software. Biplot was calculated by PC1 scores on the abscissa, and PC2 scores on the ordinate for each treatment and each variable (Yan & Rajcan, 2002), and can be expressed as:

$$\left(T_{ijk} - \bar{T}_{jk}\right) \Big/ s_{jk} = \lambda_1 \phi_{ik1} \tau_{jk1} + \lambda_2 \phi_{ik2} \tau_{jk2} + \varepsilon_{ijk}$$

in which: T_{ijk} is the average value of the combination of genotype and year ik, for trait j; $\bar{T}_{jk}$ is the average value of the combination of trait and year jk over all genotypes; s_{jk} is the standard deviation of the interaction

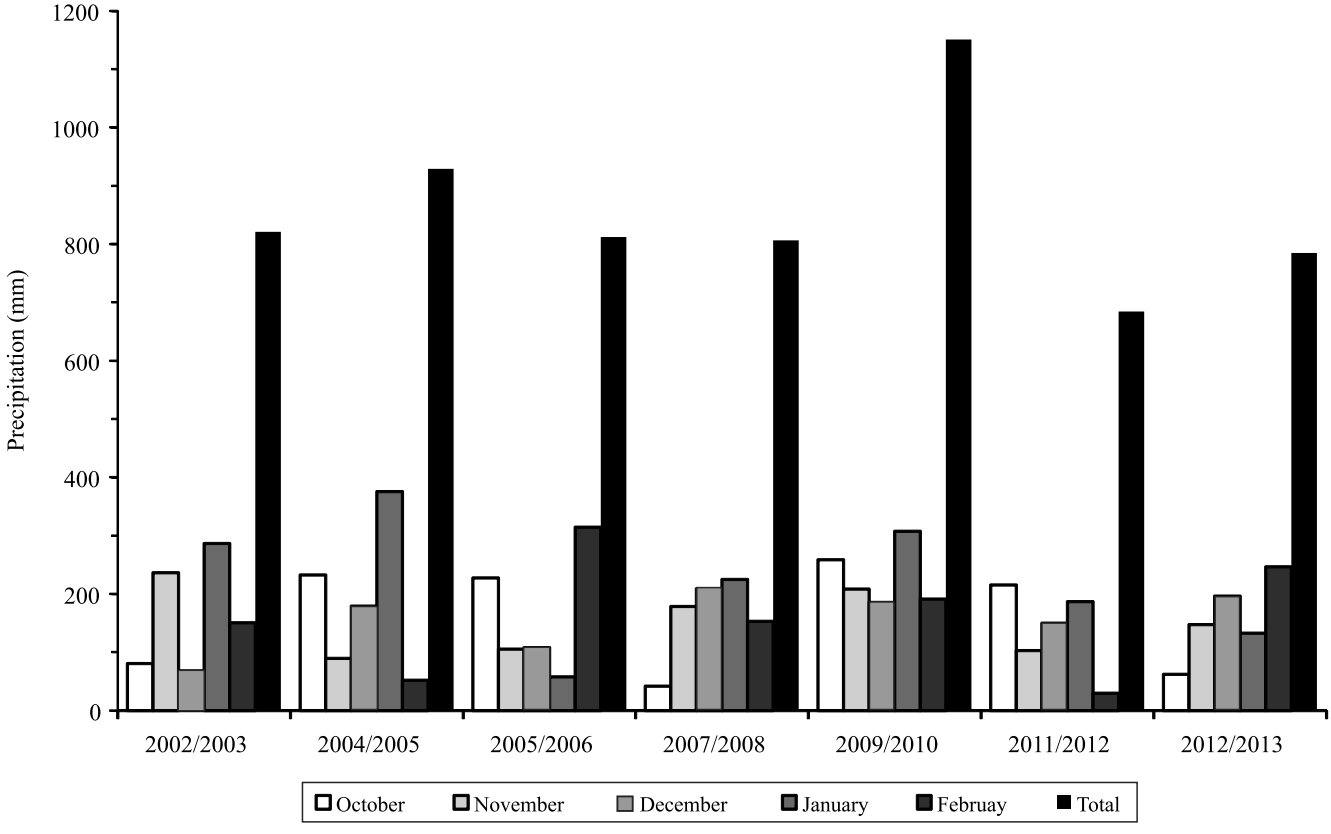

Figure 1. Accumulated precipitation (mm) for the seven growing seasons in Londrina, Brazil.

between trait j and year k, among the genotype averages; $\phi_{ik\,1}$ and $\phi_{ik\,2}$ are the PC1 and PC2 scores, respectively, for genotype i; $\tau_{jk\,1}$ and $\tau_{jk\,2}$ are the PC1 and PC2 scores, respectively, for trait j; and ε_{ijk} is the residual of the model associated with the interaction of genotype and year ik in trait j.

Results and Discussion

Pearson correlation coefficients between disease severity and yield was not significant, and it was negatively correlated (r = -0.21). Results of principal component analysis are more efficient when original data of the studied variables are correlated. Correlation between disease severity and oil content was negative and significant (r = -0.32), and between yield and oil content it was significant and positive (r = 0.28). This indicates that PCA is an option to reasonably quantify the amount of observed variables, in the complex variation structure within and among them (Silva & Padovani, 2006).

The obtained eigenvalues for the three components were, respectively, 1.5423, 0.7949 and 0.6626, totalizing 100% of the total variance (Table 2). Based on these eigenvalues, the results of PCA indicated that the first component accounted for 51.4% and the second one for 26.5% of the total variance among variables.

As to principal component analysis, the number of principal components is always equal to the considered number of variables in the research; however, the number of components or selected axes is not always equal to the maximum number of variables. Usually, the first two components explain the importance of a larger number of variables in the total variation, and the first component is the most important because it has the greatest contribution to the data variation (Silva & Padovani, 2006). In the present research, the first two principal components or two axes explained 77.9% of the total variation. Therefore the first component, by which disease severity and oil content showed the highest contribution, was the most important (Table 2). The second component represents the contribution of disease severity and yield to compare sunflower genotypes. Akinwale et al. (2014) state that no studies have been carried out to specify when the proportion of variation explained by a biplot becomes too small to make a valid conclusion; however, it is generally assumed that any proportion below 40% is too small. This shows the importance of PC1, as reported by Ullah et al. (2007), regarding that ideal sunflower cultivars should have a large PC1 score and a small (absolute) PC2 score.

Yan & Tinker (2006) developed studies on genotype x environment interaction, using GGE biplot, in order to verify the selection of the best genetic material that shows stability in different environments. One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment dataset. Many researchers find this use of a biplot intriguing, as it graphically addresses important concepts such as genotype x environment interaction, mega environment differentiation, specific adaptation, etc. In fact, GGE biplot graphic facilitates the visual evaluation of both genotype and genotype x environment interaction, showing different sunflower genotype groups based on their performance (Ullah et al., 2007).

Based on the two principal components with the three investigated variables, the polygon was formed by connecting the markers of the genotypes that were further away from the biplot origin, such that all other genotypes were contained in the polygon. Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more locations, since they had the longest distance from the origin of biplot. The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them. The equality lines divide the biplot into sectors, and the winning genotype for

Table 2. Eigenvalues and eigenvectors of principal component analysis (PCA) for Alternaria leaf spot severity (%), grain yield (kg ha^{-1}), and oil content (%) of 69 sunflower genotypes.

Component	Eigenvalue	Total (%)	Total Accumulated	Variance Accumulated	Eigenvectors (coefficients for PCA)		
					Disease severity	Yield	Oil content
PC1	1.5423	51.4122	1.5423	51.41	0.5749	-0.5374	-0.6169
PC2	0.7949	26.4980	2.3373	77.91	0.5930	0.7931	-0.1382
PC3	0.6626	22.0897	3.0000	100.00	-0.5636	0.2863	-0.7747

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each sector is the one located on the respective vertex (Yan & Tinker, 2006; Farshadfar et al., 2011).

In the biplot using the first two principal components, the variables disease severity, yield, and oil content were located on three different sectors (Figure 2), within the third and fourth concentric circles (Figure 3). The concentric circles on the biplot help to visualize the vector length (the distance from a marker to the biplot origin) (Yan et al., 2015), and also show the discriminating abilities of the variables (Jalata, 2011). Treatments with longer vectors indicate higher contributions and also higher variances. Genotypes located on the vertices close to the variables were observed as the most responsive ones (Table 3). Opposite effects were observed when genetic materials were placed on vertices located on the opposite side of the studied variables.

According to the polygonal biplot using the first two principal components, considering the variables disease severity, yield and oil content, the evaluated genotypes were divided in seven sectors (Figure 2). The first sector contained the yield vector. The genotype Dow MG52 (C9) was located on the vertex of the sector, showing 1,435 kg ha^{-1} yield and 50.55% oil content. Genotypes located closer to the origin of the biplot showed low contribution, such as 'BRS Gira 32' (F6) (Table 3). The second sector contained oil content vector, and few genotypes were located on this position, which represents high oil content (Figure 2). On the vertex of the polygon, there was the V20041 (E9), with 44.97% of oil content. The third sector represented low Alternaria leaf spot severity because it was located on the opposite side of the fifth sector, where the disease severity vector was located (Figure 2). Sunflower genotype Helio 358 (B6) was located on the vertex of the polygon (disease severity of 3.29%).

Yan & Tinker (2006) stated that the length of the genotype vector, which is the distance between a genotype and the biplot origin, measures the difference of the genotype from the "average" genotype. Therefore, genotypes or any treatment or variables with the longest vectors are either the best or the poorest genotypes. Despite being located on the vertex of the polygon, they are not always the best answer. If they are located on the left side of the biplot, these genotypes show the worst values, and care should be taken to not have an erroneous interpretation. This fact

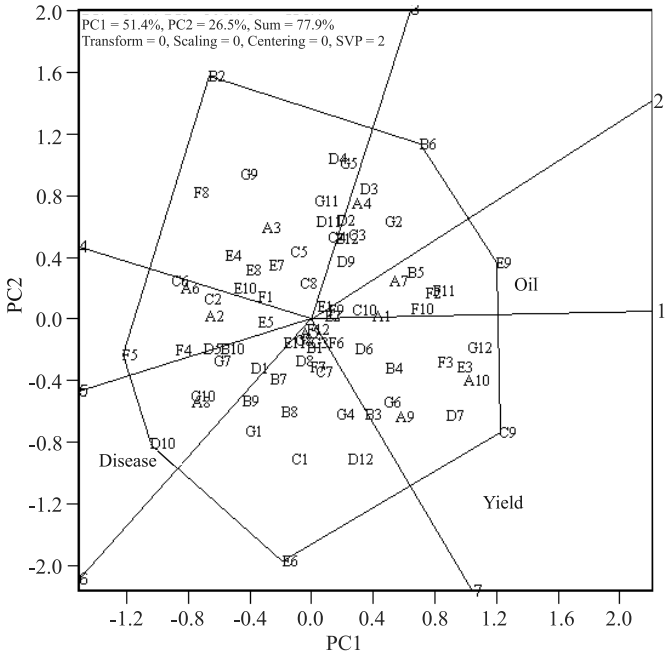

Figure 2. Polygon view of the GGE biplot based on 69 sunflower genotypes evaluated for grain yield, oil content, and reaction to Alternaria leaf spot disease, in seven growing seasons. Codes and details for the genotypes are listed in Table 1.

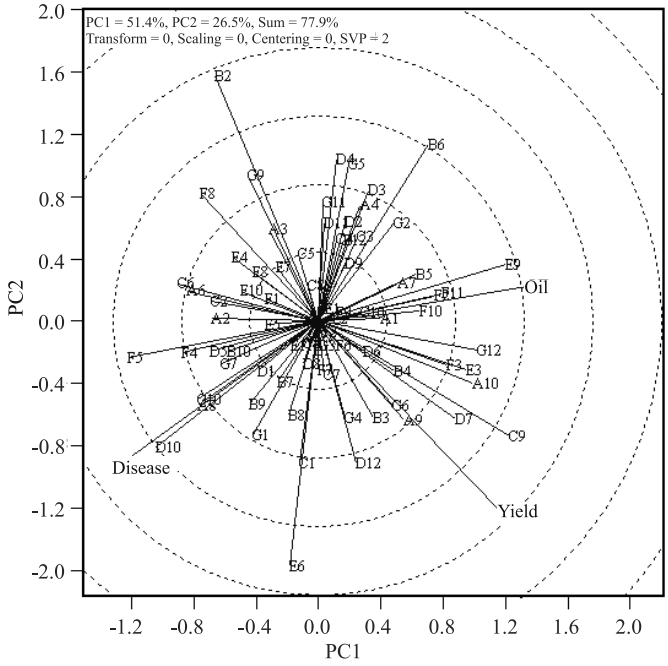

Figure 3. Vectors of the GGE biplot, based on 69 sunflower genotypes evaluated for grain yield, oil content, and reaction to Alternaria leaf spot disease in seven growing seasons. Codes and details for the genotypes are listed in Table 1.

was observed in the fourth sector (Figure 2), where the open-pollinated variety Embrapa 122 (B2) was located on the vertex of the polygon, showing a long vector (Figure 3), but its values of yield (715 kg ha^{-1}) and oil content (33.17%) were very low. Moreover, 'BRS Gira 31' (F5) was located on the vertex of the fifth sector, which represents low oil content.

The sixth sector represented high Alternaria leaf spot severity and HLA 04 (D10) was located on the sector vertex. Other genotypes located on this sector

Table 3. Contribution of grain yield (kg ha^{-1}), Alternaria leaf spot severity (%), and oil content (%) of 69 sunflower genotypes according with principal components PC1, PC2, and PC3 in descending ordination[(1)].

Ordination	PC1	Ordination	PC2	Ordination	PC3	Ordination	PC1	Ordination	PC2	Ordination	PC3
C9	6.4606	E6	10.8154	E4	9.8367	B3	0.5347	B4	0.4887	E12	0.7371
F5	6.4006	B2	10.4010	A1	6.2581	E5	0.5016	F7	0.4687	D4	0.7146
E9	6.1679	B6	5.3605	C7	4.7026	F1	0.5005	E7	0.4630	F9	0.7039
D10	4.6366	D4	4.4980	G11	4.0133	D3	0.4406	E3	0.4580	B9	0.6228
G12	4.4739	G5	4.2531	D12	3.7318	A3	0.4337	E8	0.3786	C2	0.5960
A10	4.1771	C1	3.7079	D10	3.3580	D6	0.3478	F3	0.3758	F2	0.5598
E3	3.8442	D12	3.6749	E10	3.2467	C10	0.3128	D8	0.3565	E1	0.5489
C6	3.4483	G9	3.6438	G1	2.8225	E7	0.3100	G7	0.3556	A2	0.5248
D7	3.2846	D3	2.9257	G8	2.6973	A4	0.2957	B5	0.3521	E9	0.5185
F4	3.2828	D10	2.8927	D8	2.6658	B7	0.2900	F5	0.2659	G6	0.4964
A6	3.0587	F8	2.7785	C3	2.5017	C3	0.2623	A7	0.2328	E6	0.4463
F3	2.9116	C9	2.4388	E8	2.2426	D12	0.2429	C6	0.2182	G5	0.3494
F11	2.6633	G1	2.3834	D9	2.2310	G5	0.1614	F4	0.2087	E11	0.3486
A8	2.5872	G11	2.3815	C4	2.2098	B8	0.1570	D6	0.1970	F11	0.3468
G10	2.5580	A4	2.3090	F3	2.2093	E6	0.1409	D5	0.1961	G2	0.3404
F8	2.4748	A9	1.8085	G9	2.0940	D2	0.1278	C8	0.1920	A3	0.2405
F2	2.3852	D7	1.7571	B2	2.0713	E11	0.1273	B10	0.1856	D1	0.2380
B6	2.1288	G4	1.7336	C9	1.9521	D9	0.1272	B1	0.1822	G3	0.2051
D5	2.0505	B3	1.7180	F7	1.9396	G4	0.1219	G12	0.1782	B1	0.1968
A2	2.0378	D2	1.6709	A4	1.9306	E12	0.1145	E10	0.1473	A5	0.1724
C2	2.0145	B8	1.6523	D2	1.9224	C5	0.0714	A6	0.1441	B6	0.1696
B2	1.8855	G2	1.6320	B7	1.7908	C1	0.0614	G3	0.1310	E2	0.1505
F10	1.7982	D11	1.6079	G12	1.7795	C4	0.0582	F6	0.1288	F8	0.1437
B5	1.6963	A3	1.4321	C5	1.7492	F6	0.0575	E11	0.1231	F6	0.1286
G7	1.6886	G6	1.3458	F4	1.6486	D4	0.0573	F11	0.1216	E3	0.1145
B10	1.4555	A8	1.3318	F5	1.6406	F9	0.0531	G8	0.1032	A7	0.1125
E4	1.3324	B9	1.2986	F12	1.5847	G8	0.0427	F2	0.1022	A8	0.1060
A9	1.2851	C3	1.1932	B8	1.5561	D8	0.0427	F1	0.0733	B10	0.0992
A7	1.1109	G10	1.1442	G10	1.5450	E2	0.0343	C2	0.0535	D11	0.0593
E10	1.0800	C4	1.1214	D5	1.3297	A5	0.0222	A5	0.0480	A9	0.0563
G2	1.0032	E12	1.0945	F1	1.3053	C8	0.0192	F12	0.0294	G4	0.0526
B4	0.9921	A10	0.7525	G7	1.1137	E1	0.0083	E1	0.0176	D6	0.0293
G6	0.9735	C5	0.7373	A6	1.0216	D11	0.0059	F10	0.0110	D3	0.0287
G9	0.8801	B7	0.7078	C10	1.0175	C7	0.0057	F9	0.0080	B3	0.0253
B9	0.8481	E4	0.6697	D7	0.9218	F12	0.0035	C10	0.0074	E5	0.0218
G1	0.7653	C7	0.5551	A10	0.8092	G11	0.0034	E5	0.0074	B5	0.0111
E8	0.7543	D9	0.5484	C8	0.7829	B1	0.0029	A1	0.0001	C6	0.0086
A1	0.6678	E9	0.5154	B4	0.7820	F7	0.0002	E2	0.0001	C1	0.0071
D1	0.6356	D1	0.4976	E7	0.7511	G3	0.0000	A2	0.0000	F10	0.0014

[(1)]Codes and details for the genotypes are listed in Table 1.

were Agrobel 910 (A8) and BRS Gira 36 (G10) (Figure 2).

The sunflower hybrid Dow M734 was the common genotype included in all trials; it showed a general pattern, since in four out of seven growing seasons it was located on the seventh sector (Figure 2), showing high disease severity (up to 19.25%) and high yield (up to 1,852 kg ha^{-1}). Karimizadeh et al. (2013) observed the same fact in lentil genotypes, when GGE biplots for individual years were similarly constructed and indicated, for each year, that some of the treatments fell into different sectors, and some fell into similar sectors, but the general pattern of location groupings did not vary across the years.

'BRS Gira 27' (E6) located on the vertex of the seventh sector and showed the highest yield in 2009/2010 growing season, despite the disease severity of 22.51%. In this sector, there were genotypes showing tolerance to Alternaria disease, which is the ability of plants to produce a good crop, even when they are infected with a pathogen (Agrios, 1997).

According to the agronomical performance, genotypes located on sectors 1 and 2 showed high yield and high oil content, respectively, and should be preferably selected. Genotypes showing tolerance to the disease, found on sector 7, may also be selected.

The present results have several implications for the future breeding, genotype evaluation, and recommendation of sunflower hybrids. GGE biplot has greatly helped in the accurate analysis and data interpretation from breeding and agronomic field experiments (Akinwale et al., 2014), and offered the opportunity to identify adapted sunflower genotypes for resistance to Alternaria leaf spot that can be used in sunflower breeding programs.

Conclusions

1. GGE biplot analysis allows for a meaningful and useful presentation, and is an efficient method for grouping sunflower genotypes, as a function of Alternaria leaf spot severity, yield, and oil content.

2. GGE biplot is adequate to display different sunflower genotype groups based on their agronomical performance.

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