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Indirect selection for increased oil yield in peanut: comparison selection indices and biplot analysis for simultaneous improvement multiple traits

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Abstract

The objectives of this study were to exploit information on the nature of relationships between agronomic traits and oil yield for developing selection indices as well as to compare selection indices methodology and biplot analysis as methods of simultaneous improvement of genotypes for multiple traits. Selection indices revealed that an increase in efficiency was observed over direct selection for oil yield when four oil yield contributing traits were included along with oil yield and showed that correlation coefficients between genotypic worth and each of the base indices were less than that for the optimum indices. Applying biplot analysis to the multiple trait data revealed that genotype by trait (GT) biplot graphically facilitated visual comparison of genotypes and selection. Moreover, the identified superior genotypes in both types of analyses were nearly identical. So use of biplot analysis is recommended.

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Introduction

Most of the traits of primary importance in peanut (*Arachis hypogaea* L.) are quantitative in nature and not highly heritable. Furthermore, when selecting for a primary trait such as oil yield, the selection is being done for several secondary traits that influence the primary trait rather than for the primary trait itself. Understanding that improvement of one trait may cause improvement or deterioration in associated trait(s) serves to highlight the need for simultaneous consideration of all traits that are important in a crop species (Baker, 1986).

Germplasm evaluation and variety selection must be based on multiple traits or breeding objectives (Yan and Fregeau-Reid, 2008). For most crops, although yield is the number one objective, quality is also very important (Yan and Fregeau-Reid, 2008). So, selection based on multiple traits is an inevitable issue for all breeders. Three strategies of multitrait selection are (Simmonds and Smartt, 1999): (i) tandem selection, whereby different traits are selected in different generations; (ii) independent culling, whereby multiple traits are selected simultaneously and independently; and (iii) index selection, whereby multiple traits are selected simultaneously by an index that is a linear combination of various traits. The use of a selection index was originally proposed by Smith (1936). He argued that since genotypic worth could not be directly evaluated, it might be best estimated by a linear function of observable phenotypic values. The maximum response to index selection will be achieved if the correlation between genetic worth and the index is maximized (Baker, 1986). Index selection has also become an important concept in plant breeding and has been widely used, implicitly or explicitly, for the selection of superior varieties as well as for the improvement of a complex breeding objective (Jannink *et al.*, 2000). Iroume and Knauft (1987) used the selection indices to develop selection criteria for increasing pod yield and reducing leafspot susceptibility in peanut. Many other researchers have used selection indices as an effective selection criterion in their breeding programs on different crops (Pesek and Baker, 1969; Suvantaradon *et al.*, 1975; Wells and Kofide, 1986; Vikram and Roy, 2003; Rabiei *et al.*, 2004).

Since strong, negative correlations between breeding objectives often exist, either genetically or physiologically, which makes breeding more challenging (Yan and Wallace, 1995). Because selection for the desired levels or culling for the undesired levels of one trait can mean selection against the desired levels of another trait, which can lead to the loss of useful materials or even render the selection population useless (Yan and Rajcan, 2002). Index selection can also lead to the loss of materials with desirable levels of a trait or to the retaining of materials that have serious defects for some traits (Yan and Fregeau-Reid, 2008). A genotype by trait (GT) biplot is an effective tool for exploring multitrait data (Yan and Rajcan, 2002). It graphically displays the genotype by trait pattern and allows visualization of the association among traits across the genotype and of the trait profile of the genotypes. Yan and Rajcan (2002) used a genotype × trait (GT) biplot, which is an application of the GGE biplot technique to study of the genotype × trait data. The GGE biplot methodology was developed originally for analyzing multi environment trial data (Yan *et al.*, 2000; Yan, 2001). However, it can also be equally used for all types of two-way data that assume an entry × tester structure (Yan, 2001). The genotypes can be generalized as entries and the multiple traits as testers. A GGE biplot, constructed from the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from singular value decomposition (SDV) of the tester- centered data (Yan and Kang, 2003).

Index selection has had limited use in actual plant breeding programs. Studies have been reported in peanut (Iroume and Knauft, 1987; Vikram and Roy, 2003). The various results seem to indicate that index selection for improving one trait singly would be no better than direct selection for the trait itself, but might prove useful when selecting simultaneously for more than one trait. GT biplot methodology is a one of the best methods to propose a comprehensive multitrait selection strategy that used for line selection based on multiple traits (Yan and Fregeau-Reid, 2008). The purpose of present study is i) to construct two different types of selection indices among peanut varieties in order to compare their relative efficiency, ii) to compare selection indices result with interpretation a GT biplot and iii) selection of the most desirable varieties.

Materials and methods

Field experiments and plant material

The experiment was conducted at the research farm of the Tobacco Research Institute (49^{o} 36' east latitude, 37 ^{o} 16' north longitudes), Rasht, Iran, during 2006. The experimental material consisted of 39 peanut genotypes which were provided by the Genetic Research Department of the National Plant Gene Bank of Iran (NPGBI). The names and codes of the genotypes are provided in Table 1. The experiment was laid out in a randomized complete block design with three replications. The trial field was plowed and disc harrowed few days prior to seeding. The experimental plots consisted of three rows of 3.2 m length each. Row- to- row and plant-to- plant distances was kept at 30 and 40 cm, respectively. Weeds were controlled by hand- weeding several times as required. Neither herbicides nor insecticide were used in trial as there was no need for them. Data was taken from the middle row of each plot. All measurements were performed according to instructions stated in the peanut descriptor (Anonymous, 1981). 100-grain weight, 100-pod weight, Grain Length, Grain Width, Pod Length, Pod Width, Grain: pod volume ratio, Leaflet length, Leaflet width, Plant Height, Pods per plant and oil% traits were measured.

Statistical analysis

To select those traits that would qualify to be included as independent variables in the oil yield model, stepwise regression analysis was performed. In order to test of multicollinearity, Variance Inflation Factor (VIF) for each independent trait included in the regression model was calculated:

$$VIF_j = \left(1 - R_j^2\right)^{-1}$$

Where R_j^2 is the multiple determination coefficient for regression X_j over the other p-1 independent traits. Multicollinearity is the undesirable situation where the correlations among the independent variables are strong. Multicollinearity increases the standard errors of the coefficients. In other words, multicollinearity misleadingly inflates the standard errors. If VIF for one of the variables is greater than 5 or 10, there is collinearity associated with that variable (Rezaei and Soltani, 2003).

The estimates of genotypic and phenotypic variance and heritability for each trait and covariance for each pair of traits obtained among peanut varieties were used for construction of selection indices. To evaluate the selection strategies for maximizing peanut oil and yield, different selection indices were calculated based on optimum and base indices as described by Smith (1936), Hazel (1943), Brim *et al.*, (1959) and Baker (1986). A 5% selection intensity was used to estimated expected genetic advance (k = 2.06).

Construction of selection indices

In matrix notation, an optimum selection index (*I*) takes the following form:

$$I = b'x_i$$

Where b' is the transpose vector of weights assigned to those traits in selection index and x_i is the vector of phenotypic values for traits.

The optimum indices were constructed by solving the following matrix equation:

$$b = P^{-1}Ga$$

Where *b*: vector of index coefficients, P^{-1}: inverse of the phenotypic variance- covariance matrix, *G*: genetypic variance- covariance matrix, and *a*: vector of relative economic values or weights assigned to the different traits (Smith, 1936; Brim *et al.*, 1959; Baker, 1986; Kang, 1994).

To compare indices, four different criteria were used: Correlation coefficients between genotypic worth and each index which if it is maximum, the maximum response is obtained:

$$r_{WI} = \frac{\sigma_{WI}}{\sqrt{\sigma_I^2 \sigma_W^2}} = b_{WI} \frac{\sigma_I}{\sigma_W}$$

The matrix form as follows:

$$r_{WI} = \sqrt{\frac{b'Pb}{a'Ga}}$$

The expected change in aggregate genetic advances:

$$\Delta W = k r_{WI} \sigma_W$$

The expected genetic advance in each trait on the basis of index (R_I) and efficiency of the selection indices relative to direct selection for either trait evaluated was also investigated:

$$RE = \frac{R_I}{R_A} = \frac{r_{G(A)I}}{h_{(A)}}$$

Where R_I is the expected response for trait (A) based on selection index and R_A is the expected response based on direct selection of trait (A):

$$R_I = k r_{G(A)I} \sigma_{G(A)}$$

$$R_A = k h_{(A)} \sigma_{G(A)}$$

Where $r_{G(A)I}$ is the correlation coefficient between genotypic value of trait (A) and selection index, $\sigma_{G(A)}$ is the genotypic standard deviation for trait (A) and $h_{(A)}$ is the square root of heritability of trait (A). Base index proposed by Williams (1962) uses the economic weights as index coefficients:

$$I = a'x_i$$

In this index, the correlation coefficients between index and genotypic worth is calculated in matrix notation as follows:

$$r_{WI} = \sqrt{\frac{a'Ga}{a'Pa}}$$

Where a' is the transpose vector of relative economic weights.

GGE biplot

The term GGE is the contraction of G+GE. A biplot that displays the GGE of an MET dataset is called a GGE biplot. GGE biplot model keeps G and GE together and partitions this mixture GGE into two multiplicative terms (Yan and Kang, 2003):

$$\hat{Y}_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

Where $\hat{Y}_{ij}$ is the expected yield of entry i in tester j, μ: the grand mean of all observations, β_j: the main effect of tester j, and where g_{i1} and e_{1j} are called the primary scores for entry i and tester j, respectively; g_{i2} and e_{2j}, the secondary scores for entry i and tester j, respectively; and ε_{ij} is the residue not explained by the primary and secondary effects. A GGE biplot is constructed by plotting g_{i1} against g_{i2}, and e_{1j} against e_{2j} in a single scatter plot (Yan and Kang, 2003).

The most common way to implement above equation is by subjecting the GGE data to SVD (Yan and Kang, 2003):

$$\hat{Y}_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij}$$

Where λ_1 and λ_2 are the singular values of first and second largest principal components, PC1 and PC2, respectively; the square of the singular value of a PC is the sum of squares explained by the PC; ξ_{i1} and ξ_{i2} are the eigenvectors of entry i for PC1 and PC2, respectively; and η_{1j} and η_{2j} are the eigenvectors of tester j for PC1 and PC2, respectively.

Although the GGE biplot methodology was originally proposed for analyzing multi-environment trials data for a given trait, it is equally applicable to all types of two-way data that assume an entry-by-tester structure, such as a genotype-by-trait two-way dataset (Yan and Kang, 2003). The only difference is that in genotype-by-trait data, different traits have different units, and the units need to be removed through standardization before meaningful biplot analyses can be made (Yan and Kang, 2003). Therefore, within tester standard deviation-standardized model for mean or nonreplicated data:

$$(\hat{Y}_{ij} - \mu - \beta_j)/d_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

and within tester standard error-standardized model for replicated data:

$$(\hat{Y}_{ij} - \mu - \beta_j)/s_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

are appropriate models (Yan and Kang, 2003). Genotype by trait biplots generated using GGEbiplot software (Yan, 2001)

Result and discution

Selection indices

Correlation coefficients were computed for each pair of traits and they were further partitioned into components of direct and indirect effects by path Coefficients analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959). Path coefficients analysis for oil yield indicated that oil%, 100-pod weight, grain pod ratio and grain per pod were added to the multiple regression model, as the first-order predictor variables, and had the highest direct and indirect effects on oil yield. Results from multicollinearity test showed that VIF values for the regression coefficients are in the acceptable range for the lack of multicollinearity among the independent traits (Table 2).

Table 1. Genotype code and name of 39 peanut genotypes.

Genotype code	Name	Genotype code	Name	Genotype code	Name	Genotype code	Name
A2	ICGV 92049	A12	ICGV 93163	B14	ICGV 93135	D14	ICGV 93277
A3	ICGV 92050	A14	ICGV 93171	B15	ICGV 93136	E2	ICGV 92195
A4	ICGV 92052	B4	ICGV 92022	D2	ICGV 92113	E8	ICGV 92267
A5	ICGV 92054	B5	ICGV 92023	D3	ICGV 92116	E10	ICGV 93282
A6	ICGV 92064	B6	ICGV 92027	D4	ICGV 92118	E11	ICGV 93388
A7	ICGV 92071	B7	ICGV 92028	D6	ICGV 92121	E12	ICGV 93292
A8	ICGV 92076	B10	ICGV 92040	D9	ICGV 93233	E13	ICGV 93420
A9	ICGV 93152	B11	ICGV 93128	D11	ICGV 93260	E14	ICGV 94361
A10	ICGV 93155	B12	ICGV 93133	D12	ICGV 93261	E15	Chico
A11	ICGV 93162	B13	ICGV 93134	D13	ICGV 93269		

The path analysis in this study was used for developing the selection indices, so that the cause and effect relationship between oil yield and other traits were not important for us. However, most other researchers such as Hoque *et al.* (1993), Siddique *et al.* (2006) have used path analysis for improving peanut yield. Table 3 shows the results of the path analysis for the first-order prediction variables of oil yield. To evaluate selection strategies for maximizing oil yield, selection indices were calculated based on two methods (optimum and base) for four independent traits along with oil yield with different economic weights. The vector of relative economic weights for traits are presented in Table 4 that include single values (1), phenotypic and genotypic correlation, coefficients of direct effects in path coefficients analysis, the first factor loadings from factor analysis and broad sense heritability.

Table 2. Estimated VIF value for each predictor variable in stepwise regression model.

Trait	VIF
Oil%	2.499
Grain: pod ratio (GPR)	2.269
100-pod weight (PW)	4.414
Grains per pod (GPD)	1.104

The expected change in aggregate genetic advance, the correlation coefficients between genotypic worth with each index (r_{WI}) and efficiency of selection indices relative to direct selection for both sets of selection indices are presented in Tables 5, 6, 8 and 9. The highest gain in expected genetic advance, both in base and optimum indices, was obtained when selection was based on indices 1 and 6.

Comparisons of Tables 5 and 8 indicated that correlation coefficients between genotypic worth and each of the base indices were less than that for the optimum indices. The range of index relative efficiency for indices was between -21.1 and 159.1% for optimum indices and between -40.3 and 149.2% for base indices.

Table 3. Path coefficients (underlined) and indirect effects of first-order predictor variables on oil yield.

Trait	X_1	X_2	X_3	X_4	Correlation with oil yield
Oil% (X_1)	$\underline{0.403}$	-0.008	-0.063	-0.011	0.321
GPR (X_2)	-0.011	$\underline{0.285}$	0.271	0.158	0.704
PW (X_3)	-0.054	0.162	$\underline{0.476}$	0.138	0.725
GPD (X_4)	-0.019	0.196	0.286	$\underline{0.231}$	0.694
R^2 = 0.832					Residual= 0.402

Table 4. Evaluated traits and its relative economic weights for calculating of the selection indices.

	Relative economic weight					
Trait	b_1	b_2	b_3	b_4	b_5	b_6
	Unit	Phenotypic Corr.	Genotypic Corr.	Path coefficient	Broad sense heritability	Factor loading
Oil yield	1	1	1	1	0.565	0.902
Oil%	1	0.321	0.320	0.403	0.228	0.038
GPR	1	0.705	0.614	0.285	0.284	0.843
PW	1	0.725	0.526	0.476	0.228	0.856
GPD	1	0.695	0.532	0.231	0.750	0.756

Table 5. Estimated index coefficients, expected aggregate genetic advance and estimated correlation between genotypic worth and each of the indices based on optimum Smith-Hazel index.

Trait	Index coefficients					
	b_1	b_2	b_3	b_4	b_5	b_6
Oil yield	21.60	14.53	11.35	9.40	5.32	16.13
Oil%	-0.50	-0.42	-0.31	-0.20	-0.12	-0.56
GPR	0.48	0.37	0.27	0.22	0.11	0.46
PW	0.21	0.15	0.12	0.00	0.05	0.18
GPD	12.85	10.34	8.72	3.90	4.12	13.29
ΔW	37.28	26.92	20.90	15.77	5.49	31.76
r_{WI}	0.84	0.83	0.84	0.83	0.84	0.83
R^2	0.70	0.70	0.70	0.70	0.71	0.69

Each index has been calculated by using the economic weights presented in Table 4.

The results of efficiency of index selection relative to direct selection for either trait evaluated showed that except for selection index 4, index selection for increased oil yield, grain pod ratio and 100 grains weight of peanut genotypes would be between 5 and 62% more efficient than direct selection, depending on the trait and selection method. Comparisons of Tables 6 and 9 also showed that the use of selection indices to improve oil% and grains per pod was not effective. Moreover, on the basis of calculated selection indices three genotypes D4, B10 and B13 were selected as the superior genotypes (Tables 7 and 10).

Williams (1962) stated that comparing the corresponding correlation coefficients between genotypic worth and each index can be obtained the efficiency of optimum indices relative to base indices (Table 11). As can be seen in Table 11, the efficiencies of optimum indices compared with base indices were higher in all cases.

Table 6. Expected genetic advance based on selection by index (RI) and estimated efficiency of selection indices to direct selection with 5% selection intensity (k = 2.06) according to optimum index method.

	Indices											
Trait	I_1		I_2		I_3		I_4		I_5		I_6	
	RE	RI	RE	RI	RE	RI	RE	RI	RE	RI	RE	RI
Oil yield	1.41	0.51	1.40	0.59	1.40	0.59	1.41	0.36	1.42	0.60	1.38	0.58
Oil%	0.11	0.13	-0.21	-0.11	-0.20	-0.24	0.77	2.66	0.16	0.16	-0.07	-0.19
GPR	1.52	11.62	1.61	10.10	1.58	10.12	0.29	2.09	1.53	12.14	1.59	11.91
PW	1.49	24.43	1.47	20.87	1.49	20.73	0.84	13.71	1.41	23.24	1.46	24.48
GPD	0.85	0.34	0.85	0.21	0.84	0.21	0.34	0.07	0.88	0.26	0.84	0.25

Each index has been calculated by using the economic weights presented in Table 4.

Table 7. Estimated index value for five of the most desirable genotypes and genotype code (in parenthesis) for optimum in.

dex						
Number	I_1	I_2	I_3	I_4	I_5	I_6
1	124.06(D4)	88.70(D4)	69.65(D4)	51.86(D4)	32.15(D4)	103.48(D4)
2	119.95(B10)	86.91(B10)	68.18(B10)	49.80(B10)	31.29(B13)	102.46(B10)
3	114.27(B13)	81.83(B13)	64.25(B13)	47.78(B13)	27.50(D9)	95.83(B13)
4	105.24(D9)	75.96(D9)	59.85(E2)	43.33(E2)	27.11(D6)	89.35(E2)
5	105.11(E2)	75.32(D6)	59.40(D9)	43.17(D6)	26.22(A8)	87.93(D9)

Table 8. Expected aggregate genetic advance and estimated correlation between genotypic worth and each of the indices based on base index method.

	Indices					
	I_1	I_2	I_3	I_4	I_5	I_6
ΔW	29.53	21.84	21.84	12.16	7.73	26.12
r_{WI}	0.66	0.67	0.67	0.64	0.68	0.68
R^2	0.44	0.46	0.46	0.41	0.47	0.46

Each index has been calculated by using the economic weights presented in Table 4.

Table 9. Expected genetic advance based on selection by index (RI) and estimated efficiency of selection indices to direct selection with 5% selection intensity (k = 2.06) according to base index method.

	Indices											
Trait	I_1		I_2		I_3		I_4		I_5		I_6	
	RE	RI	RE	RI	RE	RI	RE	RI	RE	RI	RE	RI
Oil yield	1.09	0.46	1.08	0.46	1.10	0.47	1.06	0.45	1.13	0.48	1.05	0.44
Oil%	-0.00	-0.01	-0.07	-0.25	-0.18	-0.24	0.22	0.30	-0.40	-0.05	-0.15	-0.52
GPR	1.21	8.90	1.30	9.38	1.13	9.22	0.32	2.59	1.49	9.20	1.21	9.42
PW	1.18	20.00	1.27	20.47	1.05	20.79	0.24	3.79	1.22	8.54	1.31	20.87
GPD	0.61	0.16	0.62	0.17	0.64	0.17	0.68	0.27	0.65	0.18	0.63	0.17

Each index has been calculated by using the economic weights presented in Table 4.

Table 10. Estimated index value for five of the most desirable genotypes and genotype code (in parenthesis) for base index.

Number	I_1	I_2	I_3	I_4	I_5	I_6
1	337.33(D4)	223.27(D4)	174.66(D4)	62.03(D4)	82.75(D4)	246.44(D4)
2	327.74(B10)	218.59(B10)	171.21(B10)	61.27(B13)	80.82(B10)	243.25(B10)
3	318.83(B13)	213.43(D9)	164.87(B13)	57.94(D9)	78.93(D9)	235.69(A8)
4	318.06(D6)	211.44(A8)	163.62(A8)	57.32(B4)	78.72(B13)	234.48(D9)
5	316.04(A8)	208.96(B13)	163.57(D6)	57.28(A11)	77.60(D6)	230.52(D6)

Table 11. Estimated relative efficiency of optimum selection indices over base indices.

	Indices					
	I_1	I_2	I_3	I_4	I_5	I_6

$RE = \frac{r_{WI_O}}{r_{WI_B}}$	1.26	1.23	1.23	1.27	1.22	1.21

Each index has been calculated by using the economic weights presented in Table 4.

In conclusion, results derived from all indices indicated that among evaluated indices, one and factor loading weights that assigned as relative economic weights would improve peanut oil yield using either the optimum index or base index.

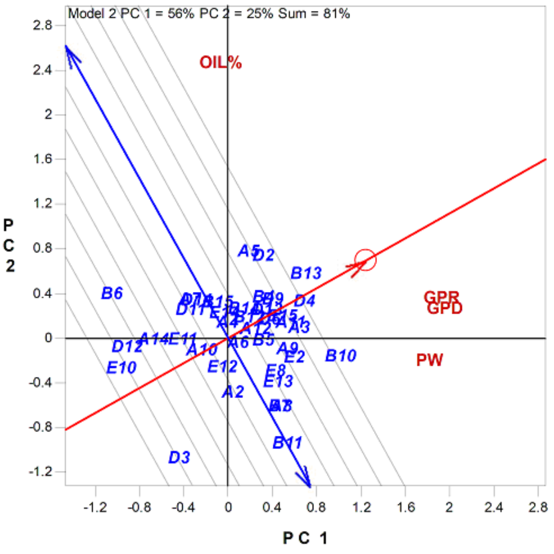

Fig. 1. The average tester or ATC view of the GGE biplot. The symbol of genotypes and traits are the same as Tables 1 and 2

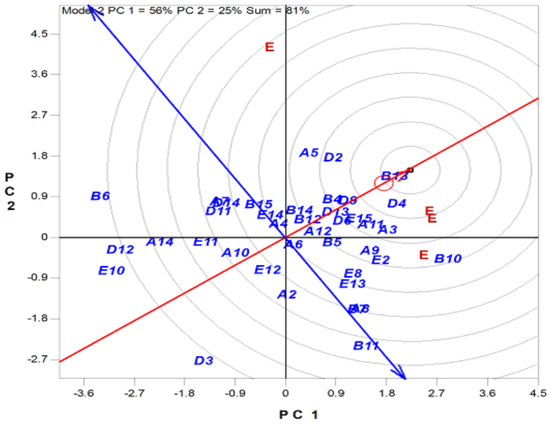

Fig. 2. Comparison of all genotypes with the ideal cultivar. The genotypes are ranked based on their distance from the ideal cultivar. The symbol of genotypes and traits are the same as Tables 1 and 2

GT biplot

The GT biplot (Fig. 1) displays 81% of information in the standardized data (within tester standard error-standardized model) of the 39 genotypes four independent trait. Evaluation of the genotypes based on average trait is achieved by drawing an average tester coordinate (ATC) on the biplot (Fig. 1)(Yan and Kang, 2003). An average trait, represented by the small circle, is defined by the mean PC1 and PC2 scores of the traits. The line that passes through the biplot origin and the average trait may be called the average trait axis is the abscissa of the ATC. Projections of genotype markers onto this axis should, therefore, approximate the mean yield of the genotypes (Yan and Kang, 2003). Thus, the cultivars are ranked along the ATC abscissa, with the arrow pointing to higher mean performance. Cultivar B13 was clearly the superior cultivar, on average, followed by B10 and D4, etc. The small circle in Figure 2, which is located on the ATC abscissa and with an arrow pointing to it, represents the ideal cultivar. Such an ideal genotype rarely exists in reality. Nevertheless, it can be used as a reference for cultivar evaluation. The plot distance between any cultivar and this ideal cultivar can be used as a measure of its desirability (Yan and Kang, 2003). The concentric circles, taking the ideal cultivar as the center, help in visualizing the distance between all cultivars and the ideal cultivar (Figure 5.23). Hence, B13 is closet to the ideal cultivar, and therefore, most desirable of all the tested cultivars. It is followed by D4, D9 and etc.

Conclusion

Because most breeding programs are concerned with simultaneous improvement of several traits, the selection index has become the best alternative, provided that reliable estimates of genetic and phenotypic variances and covariances are available and appropriate economic weights of each trait can be determined. It is important to note that the selection indices results were determined by the weights given to each of the traits. These weights are somewhat subjective and depend on the breeding objectives.

Applying biplot analysis to the multiple trait data revealed that genotype by trait (GT) biplot graphically facilitated visual comparison of genotypes and selection. Although the identified superior genotypes in each methodology was nearly identical, but because of additional information are not necessary, biplot methodology is a very simple and fast method. Therefore, use of GGE biplot to identify superior genotypes for simultaneous improvement of several traits, is recommended.

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