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Genotype by Environment (G×E) Interaction and Stability in Safflower (*Carthamus tinctorious* L.)

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Abstract: The objective of this study was to evaluate G×E interactions and yield stability in multi environmental trials across wide ecological locations in Kenya. Thirty-six safflower accessions were evaluated for phenotypic traits at 4 locations namely Katumani, Kinamba, Lanet and Naivasha for two long rain seasons in two years using 7 yield components. The experimental design was a Partially Balanced Lattice design with 3 replications. Analysis of variance (ANOVA) and Principal Component Analysis (PCA) were applied for evaluation of G×E interaction, genotype classifications and stability. The ANOVA showed highly significant differences ($p<0.01$) among genotypes and locations as well as significant G×L and L×Y interactions for all yield components. The first 3 PC accounted for 79% of the total variability in morphological traits. Classification based on the first three principal components showed accessions from Asia (46, 20, 44, 19, 51, 57, 58, 41, 1, 2, 52) tended to group together however a misclassification was found where they also grouped with those of Chinese, Mexican, American and Australian origin. Analysis of G×E interaction could serve in identification of high yielding genotypes with stable performance. Different genotypes reacted differently to varying seasons as indicated by the high significant G×E interaction hence environmental effects are important in understanding plant growth and should be given consideration in safflower breeding programs.

Key words: PCA, capitula, morphological traits, eigen values, genotypes, accessions

INTRODUCTION

Due to G × E interactions, yield trials over sites and years are an integral part of any plant-breeding program and are used to evaluate the yield potential, adaptability and stability of selected lines. Therefore identification of germplasm with broad adaptation would be helpful in development of improved cultivars. Morphological characters are limited in number and often do not reliably portray genetic relationships since G×E interaction reduces the rate of genetic improvement (De Lacy *et al*., 1996). This makes it necessary to test selections over several seasons and sites (Yau and Ortiz-Ferrara, 1994). In crop improvement programs, G×E interactions make cultivar selection difficult as they change the genotypic composition of selected or rejected groups in a given environment (Alagarswamy and Chandra, 1998; Berdahl *et al*., 1999). The quantitative G×E interactions, indicating the magnitude of differences among genotypes over environments, become important when disseminating improved germplasm. Numerous statistical techniques have been proposed to study G×E interaction. Using the PCA Model, G×E interaction can be quantified. From the biplot, genotypes and environments located near the origin are more stable and those located far away from the origin are more responsive (Yau and Hunt, 1998). Genotypes and environments that fall into the same sector interact positively, while those falling in opposite sectors interact negatively. If they fall into adjacent sectors, the interaction is more complex. When the total response across environments is considered as a combination of G×E effects and if G×E accounts for a greater degree of variance than G alone, it actually means some genotypes are less stable than others (Scott *et al*., 1997). This study was conducted to determine the environmental effects on 36 safflower introductions and to characterize genotypic differences and stabilities.

MATERIALS AND METHODS

Thirty-six safflower accessions were evaluated for phenotypic traits at 4 locations namely Katumani,

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Kinamba, Lanet and Naivasha for two long rain seasons in two years. The experimental design was a Partially Balanced Lattice design (6×6) with 3 replications. There were 6 blocks in each replication and each block had 6 accessions. Each plot had 4 rows of 6 m with a spacing of 40 cm and 30 cm between plants. Recommended crop management practices were followed to raise the crop at all sites. Plots were kept weed, pest and disease free until harvest.

Phenotypic diversity: All accessions were characterized for different morphological traits from seedling to harvest. Several characters were recorded per accession and replication at three growth stages (vegetative, flowering and ripening).

Data collected: At physiological maturity, five plants were sampled/plot. These were cut at ground level and used to determine: The number of primary and secondary branches/plant, number of capitula/plant, number of effective capitula/plant, number of seeds/capitulum, head diameter, mean weight of 100 seeds (taken at 6% moisture content) and seed yield/plant. The seed yield plot (g) m^{-2} was obtained from the total weight of two middle rows plus the weight of the sample.

Data analysis: Seeds were dried in the shade for 2 weeks prior to shelling. The combined two-way analysis of variance for all the traits recorded was computed using Statistical Analysis System (SAS 6.12, 1996 software) to assess the nature of differences among genotypes (G), among environments (E) and the interactions (G×E). Replications and locations were considered as random effects whereas genotypes were considered as fixed effects. Means were separated using DMR at ($p \leq 0.05$). The mean squares due to location-entry interaction being used as the error variance. Quantitative data was standardized (mean zero and variance one), to give each descriptor an equal weighting in analysis (Harch *et al*., 1996). PCA was conducted to determine the relative importance of classification variables. The seven morphological characters, which showed significant correlation, were used to perform PCA in both years.

RESULTS AND DISCUSSION

Pooled analysis of variance indicated significant ($p \leq 0.01$) differences among genotypes suggesting the presence of variability among genotypes and among environments (Table 1).

Eigen values from the first, second and third principal component axis contributed to 45, 19 and 15%, respectively of the total variance. Thus the first 3 PC accounted for 79% of the total variability in morphological traits (Table 2).

Different responses were displayed according to safflower origins. Genotypes from different areas were grouped randomly together. Classification based on the first three PCS showed accessions from different regions tended to group together (Fig. 1-3). It revealed that accessions from Asia (46, 20, 44, 19, 51, 57, 58, 41, 1, 2, 52) tended to group together however a misclassification was found where they also grouped with those of Chinese, Mexican, American and Australian origin. The relative magnitude of eigen vectors from the first PCA indicates that; secondary branches, number of capitula, effective capitula and primary branches contributed positively to PC1.

In contrast, seeds/capitulum contributed negatively to PC1 (Table 1). PC 2 exhibited 19% of the total morphological variability and was positively associated with seeds/capitulum; yield/plant and 100 seed weight. Where as the number of capitula/plant was negatively associated with PC2.

PC3 had 15% of the total variation and was a measure of yield/plant and primary branches. Secondary branches, capitula/plant, effective capitula, 100 seed weight and seeds/capitula were negatively associated with PC3. Biplots from PCA visually demonstrate which genotypes have a strong environmental interaction and which are stable across environments. From the biplots, one can tell which genotypes were relatively stable across environments. Genotypes located near the origin are more stable while those located far away from the origin are more responsive. Genotypes that fall in the same sector interact positively while those that fall in the opposite sector interact negatively. Laurentin and Montilla (1999) and Rabbani *et al*. (1998), have reported similar results.

From the ANOVA (Table 2), environmental variance was greatest and highly significant ($p<0.01$) for all components except the yield/plot. The significant G×E interaction indicates the existence of a wide range of variations between genotypes and between seasons and that different genotypes reacted differently to varying seasons. This information shows that safflower genotypes responded to G×E interaction over the environments. Similar results were observed by (Singh *et al*., 2004). If the total genotypic response is

Table 1: Variances of various safflower yield and yield components in 2002 and 2003

Source	df	1^0 branches	2^0 branches	No. capitula	Effective capitula	Head diameter
Locations (L)	3	1673.7**	14656.3**	32086.3**	14007.6**	5.1**
Years (Y)	1	968.2**	6157.3**	14365.2**	5033.4**	5.5**
Genotypes (G)	35	6.6**	91.3**	150.8**	89.1**	0.2**
Replications	16	20.5**	60.6**	131.3**	89.5**	0.2**
Blocks	17	2.6	32.4**	59.5**	33.2**	0.1*
L×Y	3	948.0**	9901.2**	21397.9**	10263.5**	1.6**
G×Y	35	5.1*	63.9**	213.3**	108.7**	0.2**
G×L	105	7.8**	50.5**	77.5**	44.9**	0.1**
G×Y×L	105	7.2**	41.0**	133.8**	68.4**	0.1**
Error	543	1636.7	2827.7	7416.3	6898.8	20.1
Total	863					

Table 1: Continued

Source	df	Yield/plant	Seeds/capitulum	100 Seed weight	Yield/plot
Locations (L)	3	3814.1**	4338.6**	1179.4**	1921461.1**
Years (Y)	1	33.0	3333.1**	2109.1**	1060641.2**
Genotypes (G)	35	117.8**	1823.8**	6039.1**	187966.2**
Replications	16	24.3**	72.1**	97.3**	57142.7**
Blocks	17	50.9**	27.1**	168.1**	43993.2
L×Y	3	1168.6**	127.4**	408.5**	21489.9**
G×Y	35	45.5**	64.2**	164.7**	11524.4
G×L	105	156.6**	74.3**	198.0**	19696.4**
G×Y×L	105	43.8**	54.8**	111.4**	7641.4
Error	543	4854.4	6140.9	6020.8	4630698.3
Total	863				

*, ** Significant at 5 and 1% level of probability, respectively using the F-test

Table 2: Eigenvalue and eigenvectors from the seven-selected principal components axis for traits used to classify 36 safflower accessions in 2002 and 2003

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1^0 branches	0.366	0.237	0.348	0.675	-0.332	-0.357	-0.012
2^0 branches	0.517	0.063	-0.032	0.013	-0.270	0.801	0.112
No capitula/plant	0.515	-0.021	-0.254	-0.081	0.285	-0.138	-0.750
Effective Capitula/plant	0.488	0.093	-0.342	-0.103	0.336	-0.312	0.644
Yield/plant	0.171	0.316	0.762	-0.460	0.279	-0.005	0.007
Seeds/capitulum	-0.255	0.595	-0.134	0.419	0.546	0.295	-0.038
100 Seed weight	0.078	0.312	-0.690	0.372	0.497	0.165	0.086
Eigen value	3.145	1.372	1.003	0.698	0.513	0.177	0.092
Cummulative contribution (%)	45.000	64.000	79.000	89.000	96.000	99.000	1.0000

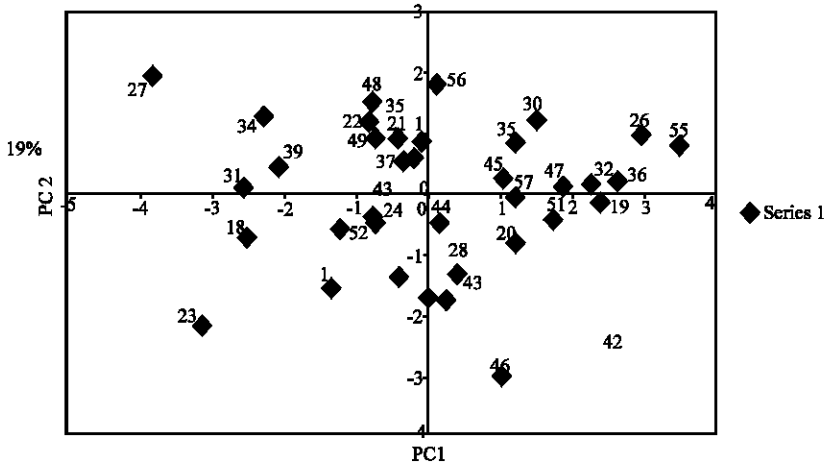

Fig. 1: 1st and 2nd PCA plot for 36 accessions in 2002 and 2003

considered as a combination of G and G × E effects, then the former was greater for primary branches, yield/plant and yield/plot. A greater part of the variance for these characters was contributed by the genotype, which means some genotypes were less stable than others. A similar trend was observed by (Scott *et al*., 1997). Hence environmental effects are important in understanding plant growth and should be given consideration in safflower breeding programs.

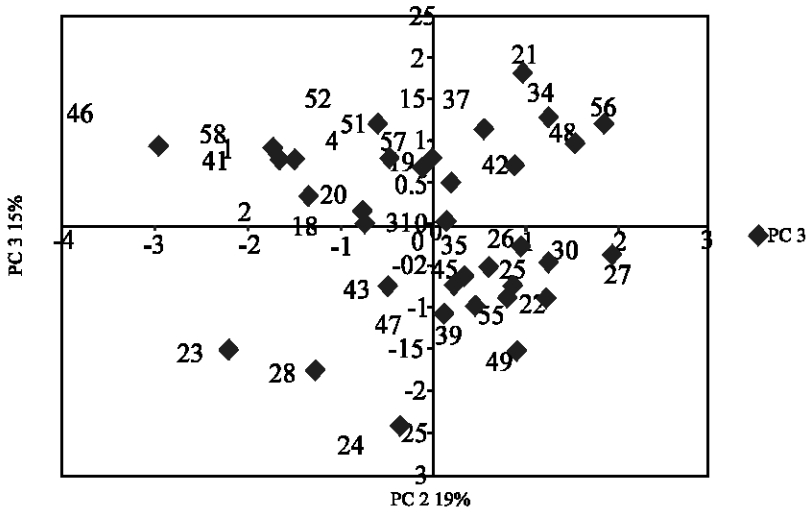

Fig. 2: 2nd and 3rd PCA plot for 36 accessions in 2002 and 2003

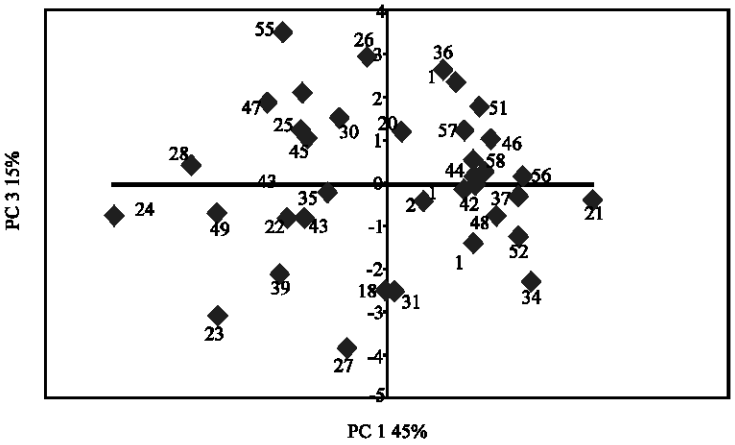

Fig. 3: 1st and 3rd PCA plot for 36 safflower accessions in 2002 and 2003

CONCLUSIONS

The first 3 PC accounted for most of the variability (79%) in morphological traits. Accessions from the same area tended to group together but occasionally a misclassification occurred.

Biplots revealed that stable genotypes tended to cluster around the origin while those found far away from the origin tend to be move responsive (Fig. 1-3). Genotypes that fall in the same sector interact positively while those that all in the opposite sector interact negatively.

These results emphasize significant G × E effects and the necessity for multiple environmental testing through time and space so as to characterize genotypic differences and stabilities. It is essential to identify safflower genotypes, which manifest relatively low G × E interactions with stable yields in test environments. Genotypes 44, 34 and 35 are likely to be stable.

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