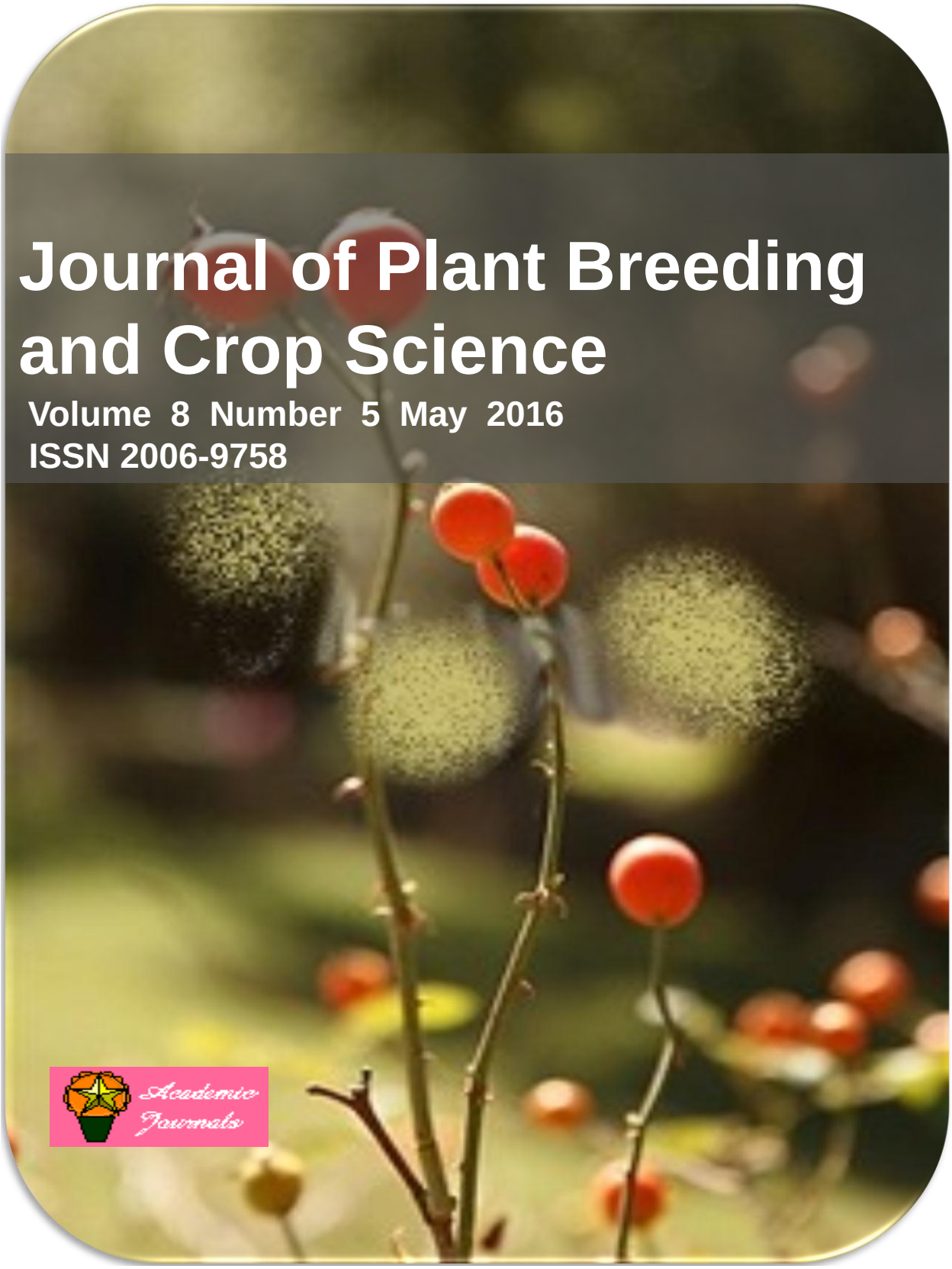

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Table of Contents: Volume 8 Number 5 May, 2016

ARTICLES

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Full Length Research Paper

Selection of cooking banana genotypes for yield and black Sigatoka resistance in different locations in Uganda

Robooni Tumuhimbise[1]*, Henry Buregyeya[1], Alex Barekye[1], Reuben T. Ssali[1], David Talengera[1], Jerome Kubiriba[1], Sedrach Muhangi[1], Betty Namagembe[1], Priver Namanya[1], Geofrey Arinaitwe[1], Wilberforce K. Tushemereirwe[1], Deborah Karamura[2] and Eldad Karamura[2]

[1]National Banana Research Program, National Agricultural Research Organization, P. O. Box 7065, Kampala, Uganda.
[2]Bioversity International, Box 24384, Kampala, Uganda.

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It is imperative to systematically evaluate new banana genotypes in different locations before national release. This enables selection and recommendation of superior genotypes as new varieties for a wider range of environments. The objective of the present study was to select banana genotypes with stable and high performance for bunch yield and leaf black Sigatoka resistance. Eleven cooking banana genotypes developed by the Uganda National Agricultural Research Organization in collaboration with Bioversity International, and two check varieties were evaluated in multi-location preliminary yield trials in Uganda. Data collected were analyzed using Additive Main Effects and Multiplicative Interaction (AMMI) model, AMMI Stability Value, and Genotype Selection Index (GSI). Genotype × location interaction was significant for all the traits assessed. Most of the new genotypes had low interaction effects with locations for bunch yield (69.2%) and black Sigatoka (92.3%). The most stable genotypes for bunch yield were NABIO815, NABIO1117, NABIO216 and NABIO306 whereas for black Sigatoka resistance, were NABIO1011, NABIO815, NABIO1009 and NABIO216. Using the GSI that defines the most desirable genotypes as those that combine high agronomic performance and stability across environments, four genotypes (NABIO306, NABIO1011, NABIO808 and NABIO1009) were selected. These genotypes, in addition to their high performance for agronomic traits and stability, had soft and yellow fruit pulp on cooking, and will be advanced on farm for further evaluation.

Key words: Banana breeding, AMMI, AMMI stability value, genotype selection index.

INTRODUCTION

Banana, including plantains (*Musa* spp.) is an important food and income generating crop in most tropical and subtropical regions of the world. In the Eastern Africa region, banana plays a major role in the diet of millions of

*Corresponding author. E-mail: rtumuhimbise@kari.go.ug. Tel: +256778455710.

people, providing up to one fifth of total calorie consumption per capita. In Uganda, banana ranks first in terms of area occupied, total production and per capita consumption (FAOSTAT, 2012). The crop is grown by over 75% of smallholder farmers owing to its unique advantages of producing acceptable yields amidst erratic rainfall, and a perennial nature coupled with an all-year-round fruiting character (Tushemereirwe et al., 2015). These attributes characterize banana as an ideal crop for household food, nutrition and income security.

Despite these benefits, banana productivity in Uganda is as low as ~ 9.2 t/ha and severely declining (FAOSTAT, 2012), although it is known that it could reach ~ 60 t/ha. Severe decline in yields is aggravated by a number of factors, key of which are: declining soil fertility, pests (weevils and nematodes) and diseases, especially black Sigatoka. Black Sigatoka, a leaf spot disease caused by *Mycosphaerella fijiensis* Morelet, causes substantial yield loss in banana production (Arzanlou et al., 2007; Daniells, 2009). This occurs because the disease attacks the leaves causing a decrease in functional leaf area. The reduction in functional leaf area results in a decline in the quality and quantity of the fruit since the fruits of infected plants ripen prematurely before proper filling (Barekye, 2009). The disease is reported to cause a yield loss of 30 to 50% on bananas (Barekye et al., 2011). For improved banana yields and sustainable food security of smallholder farmers in Uganda that largely depend on bananas, there is a need to address black Sigatoka disease.

There are several potential technology-based interventions for increasing banana yields, however, host plant resistance is the most appropriate and cost effective intervention (Tushemereirwe et al., 2015). It, in addition, offers significant spill over benefits for human health and positive environmental impacts. As a result, the Uganda National Agricultural Research Organization (NARO) through its National Banana Research Program (NBRP) and research partners, especially the International Institute of Tropical Agriculture and Bioversity International are jointly breeding banana for improved yields.

The NBRP through its Banana Conventional Breeding Unit generates banana genotypes through controlled pollination (Tenkouano et al., 2011). The genotypes generated are taken through three key evaluation and selection stages before release as new varieties. The three evaluation and selection stages are:

1. Early evaluation trial (EET),
2. Preliminary yield trial (PYT)
3. On farm trial.

Early evaluation trial stage involves the evaluation and selection of single plant genotypes in non-replicated-single site trials. Each genotype under evaluation is considered a potential variety. Selection of individual genotypes for advancement to PYT is based on high heritability traits such as plant type, bunch orientation, fruit pulp colour on cooking, and reaction of genotypes to prevalent diseases, especially black Sigatoka. Preliminary yield trial stage involves the evaluation and selection of genotypes in single or multi-location replicated trials of the few selected genotypes from EETs. Selection of genotypes at this stage of evaluation is essentially based on low heritability traits such as bunch yield and plant height. Also, reaction of genotypes to black Sigatoka, nematodes and weevils is considered. On farm trial involves the evaluation and selection of genotypes in multi-location replicated trials of the few selected genotypes from PYT. Usually, 5 to 10 farmers at each location are selected to host such trials. Selection of genotypes at this stage focuses largely on fruit sensory traits that is to say, food taste, colour, texture, smell, and mouth feel. These are judged by farmers, with the guidance of a breeder. Genotypes that are superior in the overall food acceptability, which is based on sensory traits and yield performance are recommended for national release as new varieties.

This study presents and discusses results of secondary triploid (3x) cooking banana genotypes evaluated in multi-location PYTs. Multi-locational trials have been found to be essential in plant breeding for understanding cultivar stability and yield performance across environments (Ebdon and Gauch, 2002) due to the existence of genotype x environment interaction (GEI). Genotype x environment interaction presents limitations in the selection of superior genotypes, reducing the utility of analyses of means and of inferences that would otherwise be valid (Gauch, 2006).

Genotype x environment interaction results from changes in the magnitude of differences between genotypes in different environments or from changes in the relative ranking of the genotypes (Ebdon and Gauch, 2002). Genotypes with insignificant GEI are considered to be stable (Annicchiarico et al., 2010).

The additive main effects and multiplicative interaction (AMMI) analysis is one of the widely used methods for GEI assessment (Ebdon and Gauch, 2002; Gauch, 2006). The method has been shown to be effective because it captures a large portion of the GEI sum of squares (Ebdon and Gauch, 2002). It clearly separates main and interaction effects depending on their statistical significance and presents plant breeders with different kinds of selection opportunities based on stresses that prevail in target environments (Gauch, 2006). The main objective of this study, therefore, was to select stable and high yielding-black Sigatoka resistant cooking banana genotypes with consumer-preferred traits.

MATERIALS AND METHODS

Trial sites

Trials were conducted from January, 2013 to September, 2015 at Kawanda, Mbarara, Bulindi and Nakabango agricultural research

Table 1. Properties of soil determined at planting at four experimental sites: Kawanda, Mbarara, Bulindi and Nakabango.

Variable	Soil chemical elements						
	pH	OM	N	P	Ca	Mg	K
Location	-	%	-	ppm			
Kawanda	5.1	3.8	0.21	5.7	1978.6	436.1	114.3
Mbarara	4.8	3.7	0.20	4.1	253.7	113.6	367.5
Bulindi	5.8	7.8	0.36	5.4	2302.3	904.5	305.8
Nakabango	5.7	8.0	0.35	6.6	3095.7	573.4	261.7

OM= organic matter; N= nitrogen; P= phosphorus; Ca= calcium; Mg = magnesium; K= potassium.

Table 2. Thirteen banana genotypes evaluated at four sites: Kawanda, Mbarara, Bulindi and Nakabango.

Genotype name	Pedigree	Category
NABIO1009	376K-7 x 304	Test genotype
NABIO1011	660K-1 x 1345K-1	Test genotype
NABIO1117	917k-2 x SH3362	Test genotype
NABIO216	660K-1 x 1345K-1	Test genotype
NABIO306	660K x 8075-7	Test genotype
NABIO318	4302 x 3702	Test genotype
NABIO614	917k-2 x SH3362	Test genotype
NABIO617	660K-1 x TMB2X8075-7	Test genotype
NABIO808	660K-1 x 1345K-1	Test genotype
NABIO815	376K-7 x TMB2X8075-7	Test genotype
NABIO817	222K-1 x 1345K-1	Test genotype
Kabana 6H	1201K-1 X SH3217	Check variety (hybrid)
Mbwazirume	N/A	Check variety (landrace)

stations. Kawanda is located in central Uganda at 32°36′E and 0°25′N, 1210 m above sea level (m.a.s.l.). During the trial period, mean annual rainfall and temperature were 1390 mm and 12.5°C, respectively. Nakabango is located in eastern Uganda at 33°12′E and 00°31′N, 1178 m.a.s.l. During the trial period, mean annual rainfall at the site was 1400 mm and mean temperature was 13.6°C. Bulindi is located in North western Uganda at 33°28′E and 0°28′N, 1230 m a.s.l. During the trial period, mean annual rainfall was 1150 mm and mean temperature range was 14.9°C. Mbarara is located in south western Uganda at 36°20'S and 30°37′E, 1430 m a.s.l. During the experimental period, mean annual rainfall was 1219 mm and mean temperature was 15.1°C. Soil properties for each site at planting were recorded (Table 1).

Plant germplasm

Three hundred fifty cooking banana genotypes developed by the NBRP through crossing parents of desired traits as described by Tenkouano et al. (2011), were first evaluated in an EET for three years from 2009 to 2012. Eleven genotypes selected from the EET (Table 2) were multiplied *in vitro* to generate enough plantlets for establishing replicated multi-location PYTs whose results are presented in this study. Tissue culture plantlets of Mbwazirume (landrace) and Kabana 6H (commercial hybrid variety) that were used as check cultivars were sourced locally.

Trial design

Experiments at each location were laid out in a randomized complete block design with two replications. Banana tissue culture plantlets, three months old were planted in holes (0.4 m deep and 0.6 m wide) at a spacing of 3 × 3 m, giving a plant population density of 1111 plants/ha. Before planting, 10 kg of well decomposed cow dung manure were applied in each hole. Plantlets of each genotype were established in line plots of 10 plants per line. Each replication/block was surrounded by Mbwazirume, a black Sigatoka susceptible cultivar. Two months after planting, the trials were mulched to about 0.2 m high from ground using dry grass. De-suckering was done at flowering of the mother plants to maintain the plant density and ensure that the number of bunch bearing plants was maintained at a level that reduces competition for water, light and nutrients; that is, three plants (mother, daughter and granddaughter) were maintained. The trials were regularly hand weeded and no supplemental irrigation was applied.

Data collection

At flowering, the genotypes' response to black Sigatoka infection was assessed using youngest leaf spotted (YLS) methods as described by Vakili (1968) and Carlier et al. (2002). Increasing YLS values indicate the presence of more healthy leaves on the plant, hence, greater resistance to black Sigatoka (Tenkouano et al.,

2003). At harvest, data were collected on bunch mass (kg), number of hands and fruit finger circumference. Fruit finger circumference was determined by measuring the length around the middle finger of each hand on a bunch and the average circumference calculated. Bunch yield (t/ha) was estimated from the bunch mass as follows:

$$\text{Bunch yield (t/ha)} = \frac{\text{Bunch mass(kg/plant)} \times \text{Number of plants/ha}}{1000}$$

Data analysis

The data analysed were collected for two crop cycles: 2 and 3. The two crop cycle data sets for each location were first analysed separately and found non-significantly different. Thus, combined AMMI analysis of variance (ANOVA) was conducted across locations using Genstat, version 14 (Payne et al., 2011). The AMMI ANOVA was performed using the following model:

$$Y_{ij} = \mu + g_i + e_j + \sum_{N=1}^{N} \lambda_n \alpha_{in} \gamma_{jn} + \rho_{ge} + \varepsilon_{ij}$$

Where: Y_{ij} = observed yield of genotypes; μ = grand mean; g_i = genotypic main effect; e_j = environmental main effect; N = number of PCA axes considered; λ_n = singular value of the n^{th} PCA axis; α_{in} = scores for the *i*th genotype on the n^{th} axis; and γ_{jn} = scores for the j^{th} environment on the n^{th} axis; ρ_{ge} = residual for IPCAs not fitted; ε_{ij} = error term.

Interaction patterns of the genotypes and locations were graphically represented in a biplot of the respective IPCA1 scores versus the genotype and location means for the traits assessed. In biplots, displacement in the horizontal plane reflects differences in the mean performance, whereas displacement in the vertical plane reflects differences in interaction effects (Zobel et al., 1988).

AMMI Stability Value (ASV) (Purchase et al., 2000) and Genotype Selection Index (GSI) (Farshadfar, 2008) were used to identify genotypes combining high stability and mean performance for the traits assessed. Genotype selection index for each genotype was calculated as the sum of the corresponding rankings for mean performance and ASV. AMMI stability value is a measure of the stability of a genotype (the lower the value the greater the stability) based on weighted IPCA1 and IPCA2 scores (Purchase et al., 2000). The ASV was calculated as follows:

$$\text{ASV} = \sqrt{\frac{\text{IPCA1SS}}{\text{IPCA2SS}}(\text{IPCA1score}) + (\text{IPCA2score})^2}$$

Where: ASV= AMMI stability value, IPCA1 and IPCA2: interaction principal component axes one and two, respectively and SS= sum of squares.

In selection of superior genotypes across environments, stability *per se* is not the only parameter for selection since the most stable genotypes would not necessarily give the best performance for the trait of interest. In view of that, the GSI, which combines agronomic performance across environments and stability, was used to select the most desirable genotypes. The GSI for each genotype was calculated as follows:

$$GSI_i = RY_i + RASV_i$$

Where: GSI_i = genotype selection index for the i^{th} genotype across locations for each trait;

RY_i = rank of the i^{th} genotype based on mean performance across locations; *RASV*= rank for AMMI stability value

A genotype with lowest GSI was considered to be the most stable and highest performing for that particular trait. To determine the overall best genotype that combined stability and good performance, the sum of GSI for all traits assessed was calculated. A genotype with the lowest GSI rank sum was the best in terms of the four traits assessed.

RESULTS

Variation in traits in response to genotypes and locations

Genotypes and locations in the combined AMMI ANOVA were highly significant (P < 0.001) for all the traits assessed (Table 3). Genotype × location interaction was highly significant (P < 0·001) for the number of hands, fruit finger circumference and youngest leaf spotted, and significant (P < 0·05) for bunch yield. IPCA1 was highly significant (P < 0.001) for all the traits except bunch yield (P < 0.01), and IPCA2 was highly significant (P < 0.001) for the number of hands and significant (P < 0.05) for the rest of the traits. The % treatment SS attributed to genotype for bunch yield was higher than that attributed to location or to GEI. That is, 45.3% of the treatment SS for bunch yield was attributed to genotype, 22.8% to location and 31.9% to GEI. The %treatment SS attributed to location for youngest leaf spotted was higher than that attributed to genotype or to GEI whereas for the number of hands and fruit finger circumference, the % treatment SS attributed to GEI were higher than those attributed to genotype or location.

Mean performance and genotype x location interaction for traits across locations

Bunch yield

Genotypes in quadrants II and III yielded above average (25.6 t/ha) and those in quadrants I and IV yielded below average (Figure 1). Kabana 6H, a check variety and an officially released commercial banana hybrid in Uganda had highest bunch yield (29.3 t/ha) followed closely by test genotypes *viz.* NABIO1117 (29.1 t/ha), NABIO1011 (27.3 t/ha), NABIO808 (27.2 t/ha) and NABIO617 (27.0 t/ha; Table 4). Mbwazirume, a local check variety was the worst performer for bunch yield (17.0 t/h). Genotypes NABIO815, NABIO1117, NABIO216 and NABIO306 had low IPCA1 scores for bunch yield and were accordingly the most stable genotypes for this trait. The least stable genotypes for the trait shown by high IPCA1 scores were NABIO318 and Mbwazirume. The stability of the genotypes was confirmed by the ASV (Table 4). The lower the ASV, the more stable the genotype is. Ranking

Table 3. AMMI analysis of 13 banana genotypes evaluated across four locations in Uganda for bunch yield, number of hands, fruit finger circumference and youngest leaf spotted.

Source of variation	Mean squares				
	DF	BY	NH	FC	YLS
Treatments	51	41.3***	1.59***	1.87***	7.91***
Genotypes (G)	12	79.4***	2.25***	1.67***	4.51***
Locations (E)	3	160.0***	3.89***	11.28***	89.14***
GxE Interactions	36	18.6*	1.18***	1.16***	2.28***
IPCA 1	14	24.4**	2.13***	1.56***	5.11***
IPCA 2	12	21.1*	0.74***	1.03*	0.54*
Residuals	10	7.6	0.37***	0.74	0.4
Error	48	9.6	0.04	0.37	0.5
		Sum of squares			
Source of variation	DF	BY	NH	FC	YLS
Treatments	51	2104.1	81.0	95.4	403.5
Genotypes (G)	12	953.1	27.0	20.0	54.2
Locations (E)	3	480.0	11.7	33.8	267.4
GxE Interactions	36	671.1	42.4	41.6	81.9
IPCA 1	14	342.0	29.8	21.8	71.5
IPCA 2	12	252.6	8.9	12.3	6.4
Residuals	10	76.4	3.7	7.4	4.0
Error	48	458.6	1.9	17.9	24.2
% Treatment SS due to G	12	45.3	33.3	21.0	13.4
% Treatment SS due to E	3	22.8	14.4	35.4	66.3
% Treatment SS due to GEI	36	31.9	52.3	43.6	20.3
% GEI due to IPCA1	14	51.0	70.3	52.4	87.3
% GEI SS due to IPCA2	12	37.6	21.0	29.6	7.8
% Residuals	10	11.4	8.7	17.8	4.9

DF; degrees of freedom; BY= bunch yield (t/ha); NH= number of hands; FC= fruit finger circumference (cm); YLS= youngest leaf spotted, IPCA1 and IPCA2: interaction principal component axes one and two, respectively; SS: sum of squares; ∗, ∗∗, ∗∗∗ significant at the 0.05, 0.01, and 0.001 probability level, respectively.

of genotypes based on GSI that incorporates both the mean performance and ASV rankings identified NABIO1117, NABIO306, NABIO216, Kabana 6H and NABIO808 as the genotypes combining high bunch yield and stability. Considering IPCA1, 69.2% of the genotypes had scores of less than one, implying that most of the new genotypes were stable for bunch yield. Nakabango and Mbarara had low interaction effects for bunch yield with genotypes, indicated by negligible IPCA1 scores, and were thus, stable for the trait. Kawanda and Bulindi on the other hand, had high contrasting interaction effects for the trait with genotypes and were therefore, the most unstable sites. Mbarara in general was the most yield stable site with above average performance for bunch yield.

Number of hands

Genotypes in quadrants II and III performed above average (9.1 hands) and those in quadrants I and IV performed below average (Figure 2). The first four genotypes with above average number of hands were all new hybrids *viz.* NABIO1117, NABIO817, NABIO617 and NABIO1011. These four genotypes were followed by Kabana 6H, a commercial check hybrid released by NARO in 2010. NABIO1009 and NABIO216 had the worst performance for number of hands. NABIO1117, NABIO808, NABIO306, Kabana 6H, NABIO817 and NABIO815 had low IPCA1 scores for the number of hand and were accordingly the most stable genotypes for the trait. The stability status of the genotypes indicated by the biplot (Figure 2) was confirmed by ASV (Table 5). Examination of genotypes based on GSI identified NABIO1117 followed by Kabana 6H, NABIO817 and NABIO808 as best genotypes combining high number of hands and stability. Nakabango and Mbarara had low interaction effects for number of hands with genotypes, indicated by negligible IPCA1 scores. Kawanda and

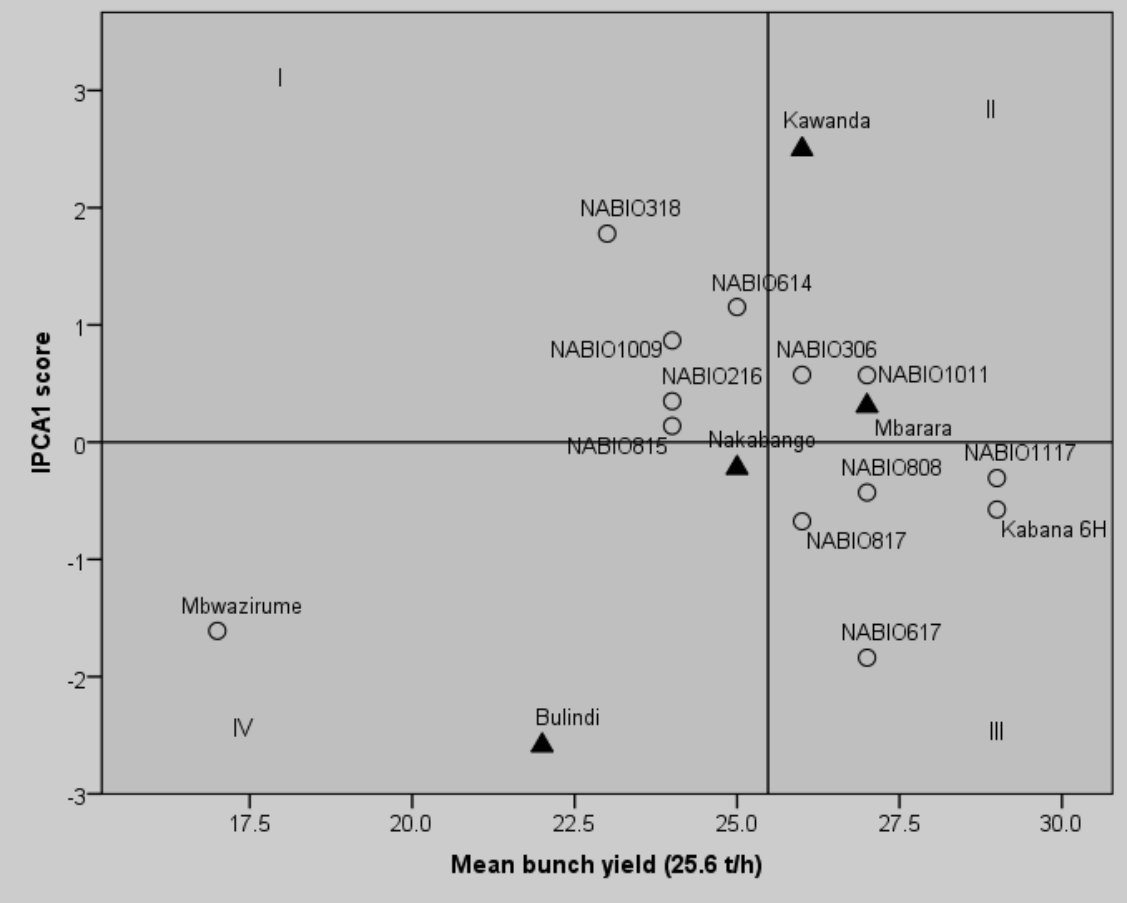

Figure 1. Biplot of mean bunch yield and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

Bulindi had high contrasting interaction effects for the number of hands with genotypes, and were therefore the most unstable sites. Although unstable, Bulindi had highest performance for the number of hands.

Fruit finger circumference

The most stable genotypes with above average performance for fruit finger circumference were NABIO306, NABIO318, NABIO617 and NABIO808. The least stable genotype with above average performance for the trait was NABIO616 (Figure 3). Mbarara and Nakabango had high contrasting interaction effects for the trait with genotypes and were therefore, the most unstable sites although heir performance was above average. The most stable sites for fruit finger circumference as indicated by very low IPCA1 scores were Kawanda and Bulindi. Ranking of genotypes based on GSI that incorporated mean performance and ASV identified NABIO306 followed by NABIO808 as the best genotypes (Table 6).

Youngest leaf spotted due to black Sigatoka

The genotypes' response to black Sigatoka infection was assessed using YLS. Genotypes in quadrants II and III were above average performance (8.3) for resistance to black Sigatoka whereas those in quadrants I and IV were below average performance (Figure 4). The top eight genotypes for black Sigatoka resistance were test genotypes *viz.* NABIO1009, NABIO1011, NABIO808, NABIO617, NABIO614, NABIO318, NABIO815 and NABIO1117. As expected, Mbwazirume, a susceptible check cultivar was the worst performer for black Sigatoka resistance (Table 7). NABIO1011, NABIO815, Kabana 6H, NABIO1009 and NABIO216 had low IPCA1 score for YLS and were accordingly the most stable genotypes for the trait. The stability of these genotypes was confirmed by ASV. The least stable genotype for the trait as indicated by high IPCA1 scores was Mbwazirume. Categorizing genotypes based on GSI identified NABIO1011 followed by NABIO 1009, NABIO815, NABIO216, NABIO306 and Kabana 6H as the best genotypes combining high resistance to black Sigatoka

Table 4. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection index for bunch yield evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV rank	GSI	GSI rank
NABIO1009	24.2	11	1.2	5	16	9
NABIO1011	27.3	3	1.2	5	8	2
NABIO1117	29.1	2	0.4	2	4	1
NABIO216	24.7	9	0.5	3	12	7
NABIO306	26.7	6	0.9	4	10	3
NABIO318	23.2	12	2.4	11	23	12
NABIO614	25.5	8	1.6	8	16	9
NABIO617	27.0	5	2.5	12	17	11
NABIO808	27.2	4	1.8	9	13	5
NABIO815	24.6	10	0.3	1	11	4
NABIO817	26.3	7	1.5	7	14	8
Kabana 6H	29.3	1	2.5	12	13	5
Mbwazirume	17.0	13	2.2	10	23	2
Mean	25.6	7.0	1.5	7	13.8	6.0
$LSD_{0.05}$	3.3	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

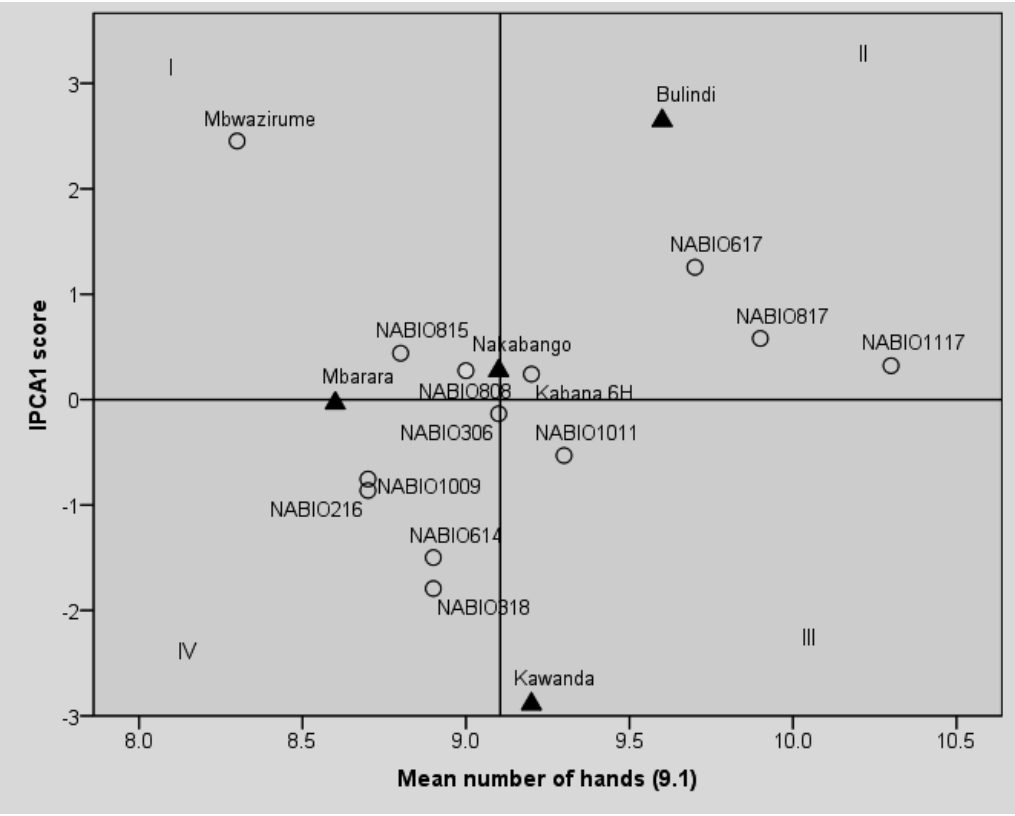

Figure 2. Biplot of mean number of hands and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

and stability. According to IPCA1 scores, all the genotypes except Mbwazirume had IPCA1 scores of less than one, implying that most of the genotypes (92.3%) were stable for black Sigatoka resistance. Kawanda and

Table 5. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection index for number of hands evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV Rank	GSI	GSI rank
NABIO1009	8.7	11	1.3	8	19	9
NABIO1011	9.3	4	1.1	6	10	4
NABIO1117	10.3	1	0.5	2	3	1
NABIO216	8.7	11	1.4	9	20	11
NABIO306	9.1	6	0.7	4	10	4
NABIO318	8.9	8	3.0	12	20	11
NABIO614	8.9	8	2.5	11	19	9
NABIO617	9.7	3	2.2	10	13	7
NABIO808	9.0	7	0.6	3	10	4
NABIO815	8.8	10	1.1	6	16	8
NABIO817	9.9	2	1.0	5	7	3
Kabana 6H	9.2	5	0.4	1	6	2
Mbwazirume	8.3	13	4.1	13	26	13
Mean	9.1	7	1.5	7	13.8	7
$LSD_{0.05}$	0.2	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

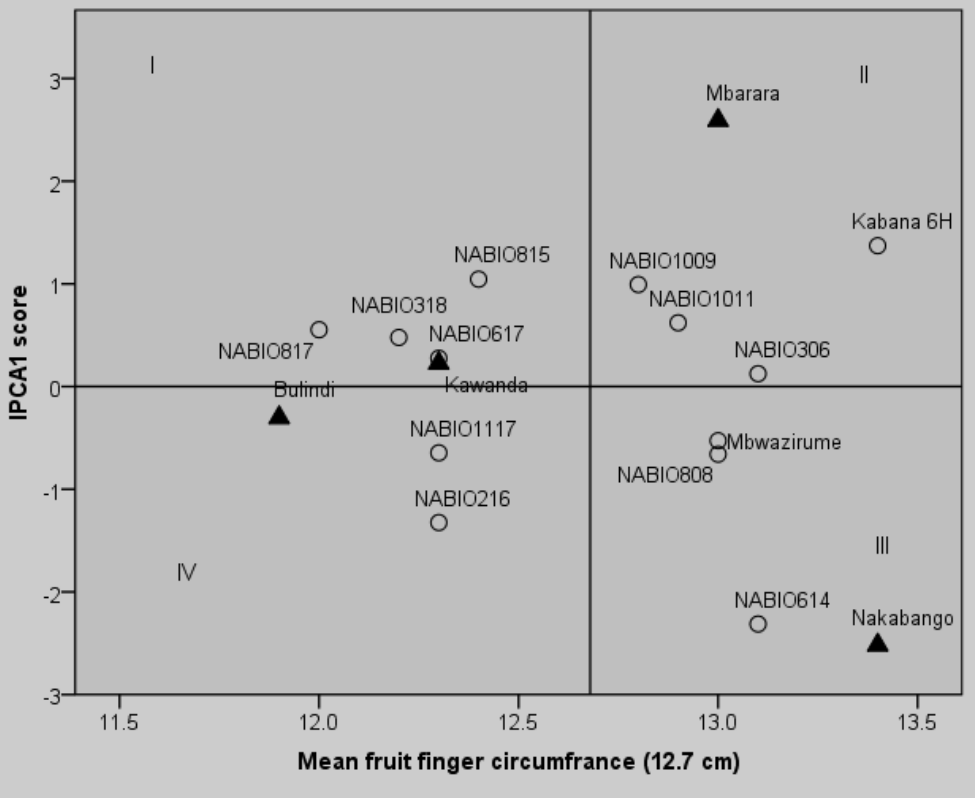

Figure 3. Biplot of mean fruit finger circumference and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

Nakabango had low interaction effects for YLS with genotypes indicated by negligible IPCA1 scores, and were therefore, stable for the trait. Mbarara and Bulindi on the other hand, had high contrasting interaction effects

Table 6. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection index for fruit finger circumference evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV Rank	GSI	GSI rank
NABIO1009	12.8	7	0.9	8	15	8
NABIO1011	12.9	6	0.9	10	16	10
NABIO1117	12.3	9	0.6	4	13	6
NABIO216	12.3	9	1.3	12	21	13
NABIO306	13.1	2	0.1	1	3	1
NABIO318	12.2	12	0.4	2	14	7
NABIO614	13.1	2	2.2	13	15	8
NABIO617	12.3	9	0.4	2	11	3
NABIO808	13.0	4	0.6	4	8	2
NABIO815	12.4	8	0.9	8	16	10
NABIO817	12.0	13	0.6	4	17	12
Kabana 6H	13.4	1	1.2	11	12	5
Mbwazirume	13.0	4	0.7	7	11	3
Mean	12.7	7	0.8	7	13.2	7
$LSD_{0.05}$	0.6	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

for the trait with genotypes and were therefore the most unstable sites.

Selection of genotypes

Genotype selection index that incorporates the rank of ASV (as an indicator of stability) and the rank of the overall trait mean values (as an indicator of performance) of genotypes in a single selection criterion, was employed to identify the desirable genotypes for all traits (Table 8). A genotype with lowest overall GSI was considered most desirable since it had a combination of overall high stability and agronomic performance for all traits. Accordingly, other than the check genotypes (Kabana 6H and Mbwazirume), four new genotypes that is, NABIO306, NABIO1011, NABIO808 and NABIO1009 were selected for advancement to on farm trials because in addition to having best performance for stability and agronomic performance for the traits assessed, they had soft and yellow fruit pulp on cooking (results not presented). Soft and yellow fruit pulp of cooking bananas are most preferred by consumers. Although NABIO1117 and NABIO815 were ranked 2nd and ^{6th} respectively, they were not selected because their fruits were seeded. The two genotypes would, however, be incorporated in the breeding program as parental germplasm. Irrespective of food sensory attributes, NABIO306, NABIO1117, NABIO1011, NABIO808, NABIO815, NABIO1009 and NABIO617 were the most stable and best performers for all traits across all environments.

DISCUSSION

Genotypes, locations and genotype x location interaction were significantly different for the four traits assessed (bunch yield, number of hands, fruit finger circumference and YLS due to black Sigatoka). Significant differences observed among genotypes for these traits indicated that significant progress would be achieved in selecting for the traits assesed. On the other hand, significant differences observed among locations for all the traits underlined the need to conduct multi-location PYTs in banana breeding in order to identify generally and specifically adapted genotypes with good performance for the traits of interest before release. Significant location effects for bunch yield, number of hands and fruit finger circumference were similarly reported by Ortiz and Cauwer (1999). Significant genotype x location interaction for the four traits assessed implied that the genotypes had different patterns of response to change in locations and should be selected at each test site.

In the AMMI ANOVA, 45.3% of the treatment SS for bunch yield was attributed to genotype, 22.8% to location and 31.9% to GEI, indicating the predominance of genetic variation among genotypes over variation among the locations or GEI for the trait. On the other hand, the contribution of GEI to treatment SS for number of hands and fruit finger circumference was higher than that of genotype and location, indicative of substantial differences in the genotype responses across locations for these traits. Therefore, selection for these traits should be done at each location to maximize potential

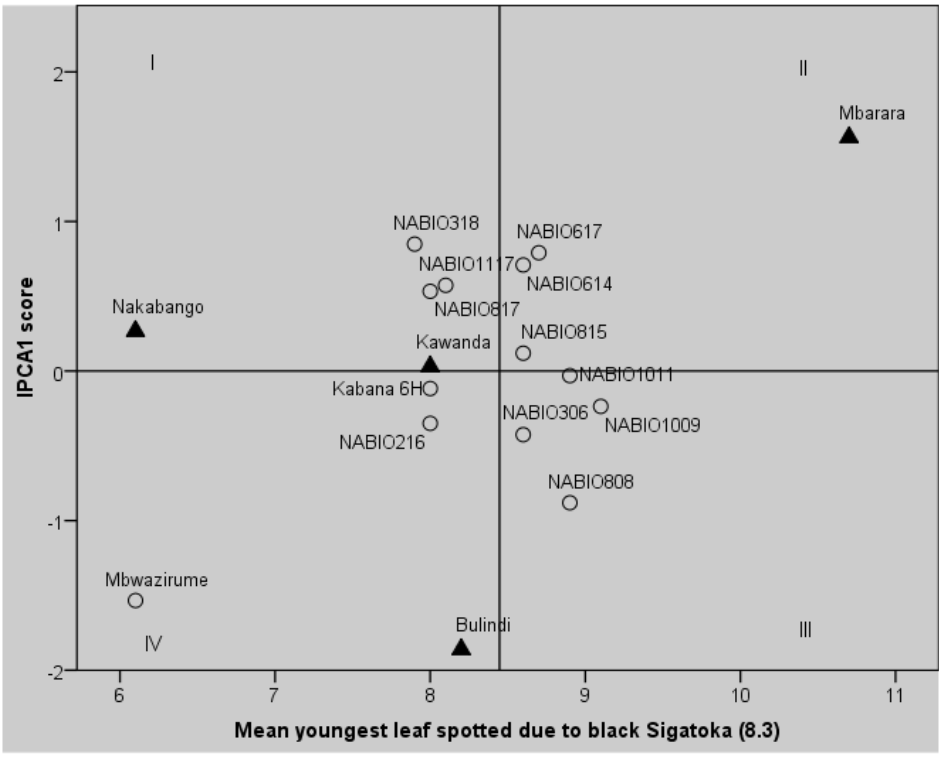

Figure 4. Biplot of mean youngest leaf spotted due to black Sigatoka and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

Table 7. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection for youngest leaf spotted evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV Rank	GSI	GSI rank
NABIO1009	9.1	1	2.7	4	5	2
NABIO1011	8.9	2	0.6	1	3	1
NABIO1117	8.1	8	6.4	8	16	10
NABIO216	8.0	9	3.9	5	14	4
NABIO306	8.6	5	4.8	6	11	4
NABIO318	7.9	12	9.5	11	23	12
NABIO614	8.6	5	7.9	9	14	6
NABIO617	8.7	4	8.8	10	14	6
NABIO808	8.9	2	9.8	12	14	6
NABIO815	8.6	5	1.3	2	7	3
NABIO817	8.0	9	6.0	7	16	10
Kabana 6H	8.0	9	1.3	2	11	4
Mbwazirume	6.1	13	17.1	13	26	13
Mean	8.3	7	6.1	7	13.4	7
$LSD_{0.05}$	0.7	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

gain.

IPCA1 was significant for all traits and IPCA2 for bunch yield, number of hands and YLS, whilst further IPCAs were not significant and captured mostly noise, thus being less helpful. This in agreement with Gauch (2006) who stated that IPCA1 and higher components in AMMI capture interaction exclusively in a monotonic sequence that decreases from the first and largest component to

Table 8. Overall ranking and selection of 13 banana genotypes by genotype selection index for bunch yield, number of hands, fruit finger circumference and youngest leaf spotted evaluated across two cycles and four locations in Uganda.

Genotype	BY		NH		FC		YLS		GSI Sum	Overall Rank	Remark[§]
	GSI	Rank	GSI	Rank	FC	Rank	YLS	Rank			
NABIO1009	16	9	19	9	15	8	5	2	55	7	S
NABIO1011	8	2	10	4	16	10	3	1	37	3	S
NABIO1117	4	1	3	1	13	6	16	10	36	2	NS
NABIO216	12	7	20	11	21	13	14	4	67	11	NS
NABIO306	10	3	10	4	3	1	11	4	34	1	S
NABIO318	23	12	20	11	14	7	23	12	80	12	NS
NABIO614	16	9	19	9	15	8	14	6	64	10	NS
NABIO617	17	11	13	7	11	3	14	6	55	7	NS
NABIO808	13	5	10	4	8	2	14	6	45	5	S
NABIO815	11	4	16	8	16	10	7	3	50	6	NS
NABIO817	14	8	7	3	17	12	16	10	54	9	NS
Kabana 6H	13	5	6	2	12	5	11	4	42	4	CV
Mbwazirume	23	2	26	13	11	3	26	13	86	13	CV

CV = check variety; S = selected, NS = not selected; BY = bunch yield (t/ha); NH = number of hands; FC = finger circumference (cm); YLS= youngest leaf spotted; and GSI = genotype selection index; Remark[§]= selection puts into consideration sensory evaluation results not presented in this paper.

the last and smallest component. Accordingly, Fikere et al. (2009) revealed that the interaction of genotypes in the field is best explained by the first two interaction principal component axes. Nevertheless, sometimes the first two IPCAs tend to rank genotypes differently giving negative and positive values. The use of ASV was therefore advocated (Farshadfar, 2008) since it gives a balanced measure between the first two IPCAs.

Based on AMMI biplots and associated IPCA1 scores, NABIO genotypes and Kabana 6H were most responsive to location effects. They represented either the best or the poorest performers in locations, corresponding to their displacement nearer to or farther from the IPCA1 origin. Nevertheless, different genotypes emerged as the best in different locations. For example, the most stable genotypes for bunch yield were: NABIO815, NABIO1117, NABIO216 and NABIO306; for number of hands: NABIO1117, NABIO808, NABIO306 and Kabana 6H; for fruit finger circumference: NABIO306, NABIO318, NABIO617 and NABIO808; and for YLS: NABIO1011, NABIO815, Kabana 6H and NABIO1009. Mbarara was the overall best site for the bunch yield due low pressure for black Sigatoka. Nakabango, on the other hand, was the second best site for bunch yield due to relatively higher soil fertility.

Farmers generally are more interested in genotypes that perform consistently better across sites, indicating preference for widely adapted genotypes (Zhang et al., 2006), and likewise, breeders would like to consider both yield and stability of performance simultaneously to reduce the effect of GEI and to make selection of genotypes more precise and refined. Although more resources may be required in breeding for specific environments, the merits of genotypes with local adaptation should also be recognized. In this study, none of the genotypes evaluated was ranked best for stability in all the four traits assessed, but widely adapted genotypes for specific traits were identified. A number of other genotypes with high trait mean values, but specifically adapted to particular environments for specific traits were also identified.

Genotype selection index helped selection of superior genotypes combining best mean performance and stability across environments since the most stable genotypes would not necessarily give the best performance for the trait of interest. In view of that, the best four genotypes selected for advancement to on farm trials were: NABIO306, NABIO1011, NABIO808 and NABIO1009. These genotypes, in addition to having better performance for all the traits assessed as well as stability, had soft and yellow fruit pulp on cooking as attributes most preferred by cooking banana consumers.

Conclusion

Genotype x location interaction was significant for all the four traits assessed, implying that the genotypes had significantly different patterns of response to change in locations and could be selected at each test site. Results suggested that it is possible to make progress in selecting high yielding banana genotypes with resistance to black sigatoka. However, the presence of significant GEI for all the traits assessed will complicate selection for these traits. The top four genotypes in terms of bunch yield, stability and preferred fruit quality traits were

selected (NABIO306, NABIO1011, NABIO808 and NABIO1009) and multiplied *in vitro* for advancement to multi-location on farm trials. Selected genotypes from farmers' fields will be recommended for national release. Multi-location preliminary yield trials are recommended in banana breeding to ensure a sound selection process that considers the effects of GEI.

Conflict of Interests

The authors have not declared any conflict of interests.

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Efficiency of selection indices in screening bread wheat lines combining drought tolerance and high yield potential

Bennani Sahar[1, 2]*, Birouk Ahmed[2], Nsarellah Naserelhaq[3], Jlibene Mohammed[4] and Ouabbou Hassan[3]

[1]National Institute of Agricultural Research, BP 578, Meknès, Morocco.
[2]Hassan II Veterinary and Agronomy Institute, BP 6202, Rabat, Morocco.
[3]National Institute of Agricultural Research, BP 589, Settat, Morocco.
[4]University Mohammed VI Polytechnique, UM6P, Benguerir, Morocco.

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Drought is the most severe production constraint for wheat worldwide. Evaluating performance of bread wheat lines and predicting drought tolerance is an essential part of the breeding process. The objective of this study is to investigate the efficiency of several indices in identifying wheat genotypes combining drought tolerance and high yield potential. Twenty-four indices, which were most frequently used in plant breeding, were compared based on grain yield of 40 bread wheat genotypes grown under two contrasting environments (stressed and non-stressed) during 2 cropping seasons 2014 and 2015. The trials were laid out as completely randomized block design of 3 replicates. Experienced stress was moderate because it caused less than 50% reduction in yield in both seasons. Analysis of variance of grain yield showed significant differences among genotypes, years, sites and genotype × site interaction. All drought indices revealed significant differences among genotypes in both seasons, except GM, SNPI and ATI. Based on correlations and principal component analysis, repeatable strong positive correlations were found between the indices (MP, MRP, REI, GMP, STI, MSTIk1, MSTIk2, HM and RDY) and grain yield under both moisture conditions during the two seasons. These indices can be considered as suitable criteria for selection of drought tolerant and high yielding genotypes under moderate stress Mediterranean environment. Moreover, these indices were able to select the highest mean yields under 20% of selection pressure with low variation across environments; especially STI, GMP and MP. The genotypes "Gladius" (9) and "AUS30355" (11) were consistently selected in both environments during two cropping seasons.

Key words: *Triticum aestivum*, drought stress, tolerance indices, grain yield.

INTRODUCTION

In the Mediterranean region, climate change is associated with more frequent and intense periods of drought as overall rainfall levels decline. The negative effect of drought stress on agriculture sector has been

*Corresponding author. E-mail: sahar.bennani@gmail.com.

qualified as a major problem in many parts of the world (Nouraein et al., 2013; Passioura, 2007), limiting the expression of crops yield potential and stability, especially in dryland areas (40% of world surface) (Karamanos et al., 2012).

Wheat is one of the most important crops for food security worldwide (Bishaw et al., 2011; Travlos, 2012). In Morocco, bread wheat is a staple food grown under various environments and agro-ecosystems. It occupies 70% of cereal cultivated area (2 Million hectare) with an average production of 2.8 Million tons. It is usually cultivated as a rain-fed crop in regions characterized by irregular annual precipitations and/or unequal distribution of rainfalls within a season (Jlibene, 2009).

Drought is a major constraint decreasing yield and potential production. Plant growth and productivity are adversely affected by water stress leading to heavy yield losses. Besides the water scarcity status, the exploration of new ways for an efficient use of water input is primordial for food security and sustainable environment. Breeding is one of the most efficient options to overcome this complex stress through the development of new varieties adapted to drought and climate instability. However, the lack of accurate reproducible screening techniques limits the success of the breeding programs (Ramirez and Kelly, 1998; Farshadfar and Elyasi, 2012; Farshadfar et al., 2012a).

Despite the lack of understanding of the drought tolerance mechanisms, the grain yield remain the basis of genotypes selection for improving drought tolerance (Talebi et al., 2009; Shirinzadeh et al., 2010; Geravandi et al., 2011; Farshadfar et al., 2012a). Some researchers believe in selection based on only favorable conditions where the low magnitude genotype × environment interaction permits to express the genetic potential yield (Richards, 1996; Rajaram and Van Ginkle, 2001; Betran et al., 2003); or only under stress conditions (Gavuzzi et al., 1997). However, high potential yield under non-stress conditions does not necessarily result in improved yield under stress conditions and genotypes with high yield may not be stress tolerant to drought and the reverse is true (Blum, 1996; Sio-Se Mardeh et al., 2006). Currently, many authors have chosen a mid-point and believe that selection considering yield under both non-stress and stress conditions is more efficient especially under unpredictable rain-fed conditions with various yearly drought scenarios (Mitra, 2001; Farshadfar et al., 2001; Moosavi et al., 2008; Mohammadi et al., 2010; Farshadfar et al., 2012a, b, 2014).

Thus, many drought indices have been proposed for screening drought tolerant genotypes based on yield under stressed and non-stressed environments (Mitra, 2001; Talebi et al., 2009; Pireivatlou et al., 2010; Mohammadi et al., 2010; Nouri et al., 2011) aiming at assisting the identification of stable, high yielding, drought tolerant genotypes: Stress susceptibility index (SSI) (Fischer and Maurer, 1978), drought response index (DRI) (Bidinger et al., 1987), relative drought index (RDI) (Fischer and Wood, 1979), mean productivity (MP), tolerance index (TOL) (Rosielle and Hamblin, 1981), drought tolerance efficiency (DTE) (Fischer and Wood, 1981), yield stability index (YSI) (Bouslama and Schapaugh, 1984), superiority index (Pi) (Lin et al., 1986), geometric mean productivity (GMP), stress tolerance index (STI) (Fernandez, 1992), drought resistance index (DI) (Lan, 1998), mean relative performance (MRP), relative efficiency index (REI) (Hossain et al., 1999), relative adaptability to drought (bN) (Karamanos and Papatheohari, 1999), modified stress tolerance indices 1 and 2 (MSTIk) (Farshadfar and Sutka, 2002), abiotic tolerance index (ATI), stress susceptibility percentage index (SSPI), stress/non stress production index (SNPI) (Moosavi et al., 2008), harmonic mean of yield (HM) (Dadbakhch et al., 2011), sensitivity drought index (SDI) (Farshadfar and Javadinia, 2011), golden mean (GM) (Moradi et al., 2012) and relative decrease in yield (RDY) (Farshadfar and Elyasi, 2012). The best indices are those which have high correlation with grain yield in both conditions and would be able to identify potential upper yielding and drought tolerant genotypes (Fernandez, 1992; Mitra, 2001; Farshadfar et al., 2001; Boussen et al., 2010).

In this perspective, the objectives of the study were to (i) investigate the repeatable ability and efficiency of 24 drought selection indices to identify the best drought tolerant and high yielding genotypes adapted to both stressed and non-stressed conditions in a Mediterranean environment, (ii) study the inter-relationships among them and (iii) identify the genotypes adapted to stressed environments.

MATERIALS AND METHODS

Plant materials and experimental design

Forty bread wheat genotypes, originating from different breeding programs, ICARDA, CIMMYT, Australia and Morocco, were chosen for evaluation based on their presumed differences for yield performance under different moisture conditions (Table 1). Those genotypes were evaluated for grain yield, in two contrasting sites, representing stressed and non-stressed conditions, during two cropping seasons. The yield data were then used to derive 24 selection indices.

Each experiment was laid out in a completely randomized block design (RCBD) with three replications. Each plot is composed of 6 rows of 5 m; with row to row distance of 0.25 m. The sowing was done in late November and harvesting in mid- May for stressed and mid-July in non-stressed experimental sites. Seeding rate was 300 grains/m². Fertilizer application (18-46-00) was 1.5 quintal/ha at planting and 1 quintal/ha (Ammonitrate 33.5%) at tillering stage. The plants were protected against foliar diseases by fungicides, and weeds were controlled manually and by herbicides when needed. Yield (t/ha) was obtained based on 9 m² of harvested plot.

Experimental sites

Two experimental stations of the National Institute of Agricultural

Table 1. List of the 40 bread wheat genotypes.

Entry code	Name	Origine	Entry code	Name	Origin
1	NEJMAH-11	ICARDA	21	SB062	CIMMYT
2	NEJMAH-14	ICARDA	22	SB109	CIMMYT
3	SHIHAB-12	ICARDA	23	SB169	CIMMYT
4	AL-ZEHRAA-2	ICARDA	24	SsrT02	CIMMYT
5	BAASHA-21	ICARDA	25	SsrT09	CIMMYT
6	AMIR-2	ICARDA	26	SsrT14	CIMMYT
7	ATTILA	CIMMYT	27	SsrT16	CIMMYT
8	SOKOLL	CIMMYT	28	SsrT17	CIMMYT
9	GLADIUS	AUSTRALIA	29	SsrW35	CIMMYT
10	AUS30354	CIMMYT	30	SsrW47	CIMMYT
11	AUS30355	CIMMYT	31	ARREHANE	Morocco
12	AUS30518	CIMMYT	32	ACHTAR	Morocco
13	AUS30523	CIMMYT	33	MARCHOUCH	Morocco
14	QG-170-4.1	CIMMYT	34	KANZ	Morocco
15	QG-58-5.1	CIMMYT	35	AMAL	Morocco
16	HARTOG	AUSTRALIA	36	MASSIRA	Morocco
17	DRYSDALE	AUSTRALIA	37	AGUILAL	Morocco
18	SB003	CIMMYT	38	BT05A104	Morocco
19	SB165	CIMMYT	39	BT05A106	Morocco
20	SB069	CIMMYT	40	RAJAE	Morocco

Research of Morocco, namely Taoujdate and Sidi El Aidi, were used as sites for experimentation, for two copping seasons 2013-2014 and 2014-2015. Taoujdate site (Fes province) represented the non-stressed or favorable environment (Altitude: 550 m, Latitude: 33°N, Longitude: 5°; long term average rainfall 500 mm; deep clayey soil (Tirs)); while Sidi El Aidi site (Settat province) represented the stressed semi-arid environment (Altitude 240 m, latitude 33°07'16'', longitude 7°37'48"W; long term average rainfall 300 mm; limestone-clay texture soil). During the rest of the document, whenever indicated, an environment will be referred to as a combination of site by year.

Calculation of indices

Drought tolerance indices per cultivar "i" were calculated based on grain yield per plot for stress (Ysi), non-stress (Ypi) environments and mean of grain yield under stressed (Ys) and non-stress conditions (Yp) as indicated in Table 2. In statistical basis, the efficiency of the drought indices will be evaluated based on their ability of discrimination between genotypes, correlation with grain yields of both environments and their efficiency to target the best high yielding and stable genotypes.

Statistical analysis

Data were subjected to analysis of variance for grain yield and drought indices using one-way ANOVA for data of each particular trial, two-way ANOVA for combined data across year, three-way ANOVA for combined data across site and year. For grain yield, the combined three way ANOVA was performed considering the effect of year, experimental site and genotype according to the model Y = year + site + bloc (site) + genotype + genotype by year + genotype by site + genotype by year by site + error. For drought indices, the combined two- way ANOVA was performed considering the effect of year and genotype according to the model Y = year + genotype + bloc + genotype by year + error, while the one way ANOVA was used for each trial separately to detect the genotypic effect per year using the model Y = genotype + bloc + error. For each combined ANOVA, the magnitude of variation attributable to each factor was estimated as percentage of variance explained (VE %) of total sum of squares.

Ranks were assigned to genotypes for each index and simple correlation analysis using Spearman's coefficient was performed to elucidate the relationships among the selection indices for each cropping season, and their association with grain yield. Based on indices formula, the genotype with the highest value for Ys, Yp, MP, MRP, REI, GMP, STI, MSTIk1, MSTIk2, HM, YI, RDI, DI, GM, SNPI, DTE and DRI and the lowest value for SSI, TOL, Pi, SDI, SSPI, ATI, RDY, b and bN received a rank 1.

Principal component (PC) analysis method based on rank correlation matrix data was used to elucidate graphically the relationships among drought indices at once. The ANOVA was performed using GENSTAT (Discovery edition 3, VSN International, UK). The correlations and PC analysis were carried out using XLSTAT (Free trial version 2015, Addinsoft, Inc., Brooklyn, NY, USA).

RESULTS AND DISCUSSION

Pattern of the cropping seasons

For the stressed site (Sidi El Aidi), the rainfall amount was about 181 and 237 mm respectively in 2014 and 2015 cropping seasons. In non-stressed conditions (Taoujdate), the rainfall amount was about 278 and 412 mm during the respective seasons 2014 and 2015. Additional irrigation (about 100 mm) was applied during

Table 2. List of the 24 drought tolerance indices and formula.

Index	Abbr.	Formula	References
Mean productivity	MP	(Ypi + Ysi) / 2	Rosielle and Hamblin, 1981
Mean relative performance	MRP	(Ysi / Ys) + (Ypi / YP)	Hossain et al., 1999
Stress susceptibility index	SSI	1-(Ysi / Ypi))/SI Where Stress intensity (SI) = 1 - (Ys / Yp)	Fischer and Maurer, 1978
Stress tolerance index	TOL	Ypi - Ysi	Rosielle and Hamblin, 1981
Geometric mean productivity	GMP	√ (Ypi x Ysi)	Fernandez, 1992
Relative efficiency index	REI	(Ysi / Ys)*(Ypi / Yp)	Hossain et al., 1999
Stress tolerance index	STI	(Ysi x Ypi) / (Yp) ²	Fernandez, 1992
Modified stress tolerance index 1	MSTIk1	((Ypi) ²/ (Yp) ²) x STI	Farshadfar and Sutka, 2002
Modified stress tolerance index 2	MSTIk2	((Ysi) ² / (Ys) ²) x STI	Farshadfar and Sutka, 2002
Harmonic mean of yield	HM	2 x (Ypi x Ysi) / (Ypi + Ysi)	Dadbakhsh et al., 2011
Coefficient of regression	b	Σ Yij Yj / Σ Y ² where i refers to genotypes and j to environment; Y is the overall mean of all genotypes in both environments.	Bansal and Sinha, 1991
Relative adaptability to drought	bN	b / a ; where b = Slope of regression model; a = intercept of regression model	Karamanos and Papatheohari, 1999
Yield Index	YI	Ysi / Ys	Gavuzzi et al., 1997; Lin et al., 1986
Superiority Index	Pi	$\sum_{j=1}^{n}$(Xij – Mj) ²/4; where Xij = Grain yield of the ith genotype in the jth environment, M = Yield of the highest yielding genotype in the environment j	Clarke et al., 1992; Lin et al., 1986
Sensitivity drought index	SDI	(Ypi - Ysi) / Ypi	Farshadfar and Javadinia, 2011
Relative drought index	RDI	(Ysi / Ypi) / (Ys/Yp)	Fischer and Wood, 1979
Drought resistance index	DI	Ysi x (Ysi / Ypi)/ (Ys)	Lan, 1998
Golden mean	GM	(Ypi + Ysi) / (Ypi - Ysi)	Moradi et al., 2012
Abiotic tolerance index	ATI	((Ypi - Ysi) / (Yp / Ys)) * (√Ypi * Ysi)	Moosavi et al., 2008
Stress Susceptibility percentage index	SSPI	((Ypi - Ysi) / (2 * Yp)) * 100	Moosavi et al., 2008
Stress/non-stress production index	SNPI	(^{3}√ (Ypi + Ysi) / (Ypi - Ysi) * ^{3}√Ypi * Ysi * Ysi)	Moosavi et al., 2008
Drought response index	DRI	(Y_A - Y_{ES}) / S_{ES} ; where YA= Yield estimate by regression in stress conditions; YES = Real yield in stress conditions; SES =Standard error of estimated grain yield of all genotypes	Bidinger et al., 1987
Relative decrease in yield	RDY	100 – ((Ysi / 100) * Ypi)	Farshadfar and Elyasi, 2012
Drought tolerance efficiency	DTE	(Ysi / Ypi) * 100	Fischer and Wood, 1981

Ysi: Yield under stress for genotype “i; Ypi: Yield under non-stress for genotype “i”; Ys: Mean of grain yield under stressed; Yp : Mean of grain yield under non-stress conditions.

critical growing stages. The drought stress occurred essentially at mid-cycle during the reproductive stage (pre-flowering and flowering) (Figure 1).

In non-stressed environment, the mean grain yield was higher during 2015 (4.49 t/ha) compared to 2014 (3.35 t/ha). However, the mean yield was 1.93 t/ha in 2014 compared to 3.05 t/ha during 2015 under stress conditions. During both seasons, the grain yield of genotypes showed greater variation under non stress compared to stress conditions. This variation can be explained by the differences in genotypes response to different moisture conditions (Mohammadi et al., 2010). Stress intensity in the first and second cropping season was respectively 0.43 (43% of yield reduction) and 0.32 (32% of reduction). Thus, the drought intensity was moderate for both seasons (below 50%). However, this index evaluates only drought stress intensity of the whole experiment and not for different genotypes.

Analysis of variance

Based on combined ANOVA, statistically significant

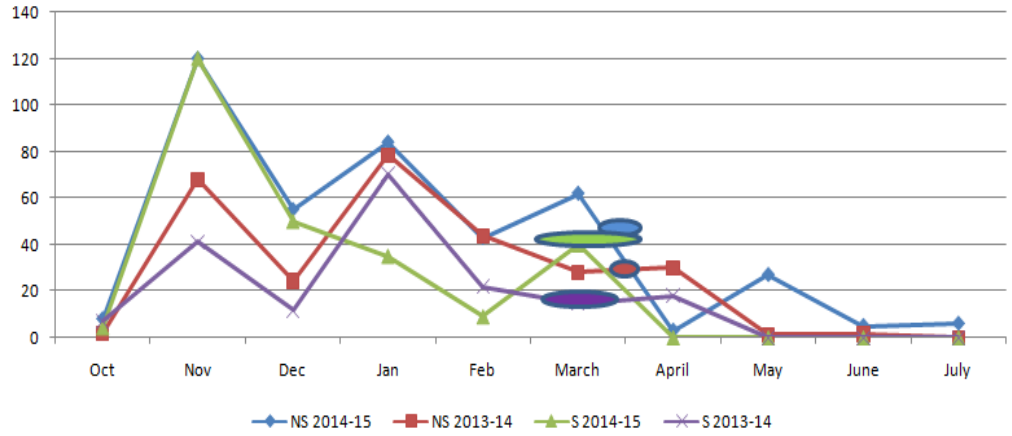

Figure 1. Rainfall amount (mm) in non-stressed (NS) and stressed (S) sites during the two cropping seasons 2013-14 and 2014-15. The oval forms refer to the timing and extension of the flowering stage.

Table 3. Combined analysis of variance for grain yield of 40 genotypes.

Source of variation	df	M.S	Percentage of variation explained (%)
Block	2	10.82	2.59
Year	1	146.68**	35.14
Site	1	255.73**	61.26
Genotype	39	1.63**	0.39
Year.Genotype	39	0.60	0.14
Year. Site	1	0.12	0.03
Site.Genotype	39	0.80*	0.19
Year. Site.Genotype	39	0.60	0.14
Residual	296(22)	0.48	0.11

*, ** Significant at 5 and 1% levels, respectively; ǂ df: degree of freedom; M.S: mean square

differences for grain yield were found among years, sites, genotypes and for genotype × site interaction. However, the other interactions year × genotype, year × site and year × site × genotype were not significant (Table 3). The magnitude of variation attributable to the years, sites and genotypes was respectively 35, 61 and 0.4% (Table 3). These results indicated that the genotypes represented a broad range of response to drought stress based on its intensity influenced by the environmental variations (Mohammadi et al., 2011; Farshadfar et al., 2012a).

The results of combined analysis of variance of selection indices are presented in Table 4. Significant differences were observed between years for ATI, DTE, GMP, HM, MP, Pi, RDY, SDI, SNPI, SSPI, STI and bN. Those indices were influenced mainly by year effect as confirmed by the percentage of explained variance per factor (Table 4); whereas, the indices DRI, MRP, MSTIk1, MSTIk2, RDI, REI, SSI, TOL and YI showed an important genotypic variation compared to the year effect (Table 4). The interaction genotype × year was significant only for SSI, Pi, ATI and RDY. Thus, those indices ranked differently the genotypes depending on the variation of stress intensity between years (Table 4).

All drought indices showed significant differences among genotypes except SNPI, b and bN during both seasons, GM which discriminated between genotypes only in 2015 and ATI which discriminated between genotypes only in 2014 season. Those results demonstrated that almost all indices revealed an important genetic diversity and were able to discriminate between the genotypes. However, the efficient indices should be also able to select the genotypes combining high yield and drought tolerance (Mitra, 2001; Farshadfar et al., 2001).

Correlation analysis

Correlation analysis revealed a positive but non-significant association between grain yield of stressed and non-stressed conditions of 0.16 and 0.3 during 2014 and 2015 seasons respectively. Correlation seemed to

Table 4. Mean Square of analysis of variance of drought tolerance indices for the 40 genotypes over and within each season 2013-14 and 2014-15.

Source of variation	Two way ANOVA						ANOVA 2014	ANOVA 2015
	Year (Y)	VE (%)	Genotype (G)	VE (%)	Y x G	VE (%)	Genotype	Genotype
MP	70.87**	94.43	0.82**	0.10	0.36	0.04	0.36**	0.83**
MRP	0.05	1.87	0.38**	14.44	0.15	5.60	0.26**	0.27**
SSI	0.23	7.77	1.10**	36.17	0.76*	24.98	7.83**	12.41*
TOL	0.007	0.02	1.63**	36.07	1.12	24.66	0.96**	1.52*
GMP	74.33**	93.55	1.03**	1.30	0.47	0.06	0.49**	1.01**
REI	0.06	0.24	0.39**	16.25	0.14	0.57	0.26**	0.27**
STI	0.47**	37.54	0.15**	12.23	0.06	0.45	0.086**	0.13**
MSTIk1	0.43	15.59	0.45**	16.30	0.16	5.89	0.27**	0.36**
MSTIk2	0.0003	0.00	1.24**	18.79	0.45	6.88	0.68*	1.01**
HM	76.16**	92.77	1.25**	1.52	0.59	0.07	0.62**	1.19**
YI	0.02	0.14	0.24**	16.33	0.11	0.70	0.17**	0.16**
Pi	25.57**	75.57	1.73**	0.51	1.16*	0.34	0.59**	2.31**
ATI	72.32**	71.70	5.23**	5.20	4.69*	4.60	2.46**	6.95
DI	0.49	22.10	0.37**	16.90	0.21	9.60	0.19*	0.32**
DRI	0.16	2.90	2.03**	27.00	0.88	11.70	1.24*	1.38**
DTE	8815**	66.70	1352.5**	10.23	879.8	6.65	652.9**	1311.5*
GM	39369	39.64	18920	19.05	19123	19.26	37596	419.5*
RDI	0.021	0.15	0.34**	24.70	0.21	15.71	0.199**	0.28*
RDY	0.29**	95.04	0.004**	0.14	0.002*	0.07	652.9**	1311.5*
SDI	0.88**	66.69	0.14**	10.23	0.09	0.66	0.066**	0.13*
SNPI	499.8**	77.02	29.58	0.45	34.25	0.53	30.54	32.54
SSPI	1656**	64.95	263.1**	10.23	177.0	0.69	212.6**	188.4*
b	0.01	-	1.49	-	-	-	-	-
bN	1.2*	-	0.23	-	-	-	-	-

*, ** Significant at 5 and 1% levels, respectively; VE (%): Percentage of variation explained.

have improved from the dry season of 2014 to the wet season of 2015 where the stressed site was 41 mm wetter than the non-stressed site of 2014. Similar findings were reported by Fernandez (1992), Clarke et al. (1992), Sio-Se Mardeh et al. (2006), Mohammadi et al. (2010), Boussen et al. (2010), Nouri et al. (2011) Dadbakhsh et al. (2011) and Farshadfar et al. (2013) suggesting that high yield under non stress condition will not result necessarily in improved yield under stress conditions (and the opposite is true) because the genes controlling yield and drought resistance/tolerance are different (Rosielle and Hamblin, 1981; Golabadi et al., 2006; Anwar et al., 2011). Thus, under such conditions, the indices correlated with both moisture conditions are the most suitable to select stable genotypes with good yield performances (Mitra, 2001; Farshadfar et al., 2001; Farshadfar et al., 2012a, b; 2013; 2014).

Correlation between grain yield and drought tolerance indices

To determine the most desirable drought tolerance criteria, the Spearman coefficient of correlation (based on ranks) between grain yield in both moisture conditions and each of the drought indices were calculated for 2013-14 (Table 5) and 2014-15 seasons (Table 6).

During 2014 (under 43% of stress intensity) (Table 5), yield under stress condition (Ys) was highly significantly and positively correlated with the indices MP, MRP, REI, SSI, TOL, GMP, STI, MSTIk1, MSTIk2, HM, YI, SDI, RDI, DI, SSPI, ATI, RDY, DTE and DRI; and moderately correlated with the coefficient of regression b. When the stress became less severe (32%) during 2015 (Table 6), the latter correlations remained the same but became stronger, except for ATI (r =0.56 in 2015 besides 0.69 in 2014). Moreover, other relationships appeared between Ys and (GM, SNPI and bN) respectively. Based on these results over both cropping seasons, significant positive repeatable correlations were found between yield under stress conditions (YS) and the drought indices (MP, MRP, REI, SSI, TOL, GMP, STI, MSTIk2, HM, YI, SDI, RDI, DI, SSPI, RDY, DTE, DRI; ATI, MSTIk1 and b). These relationships were influenced by the drought intensity (difference between Ys and Yp) and indicated that genotypes selected based on these indices are

Table 5. Spearman's rank correlation between grain yield and drought indices in 2014.

	YS	YP	MP	MRP	REI	SSI	TOL	GMP	STI	MSTIk1	MSTIk2	HM	YI
YS	1												
YP	0.16	1											
MP	0.76	0.74	1										
MRP	0.85	0.62	0.98	1									
REI	0.86	0.60	0.97	0.99	1								
SSI	0.78	-0.43	0.23	0.39	0.40	1							
TOL	0.74	0.4	0.23	0.36	0.37	0.94	1						
GMP	0.81	0.64	0.97	0.97	0.97	0.33	0.38	1					
STI	0.81	0.64	0.97	0.97	0.97	0.33	0.38	1.00	1				
MSTIk1	0.59	0.87	0.97	0.91	0.90	0.02	0.04	0.92	0.92	1			
MSTIk2	0.91	0.39	0.87	0.91	0.91	0.56	0.63	0.94	0.94	0.76	1		
HM	0.82	0.61	0.96	0.96	0.96	0.35	0.41	0.99	0.99	0.90	0.95	1	
YI	0.94	0.23	0.78	0.84	0.84	0.68	0.75	0.87	0.87	0.64	0.98	0.88	1
Pi	0.15	0.30	0.27	0.26	0.24	-0.08	-0.06	0.22	0.22	0.26	0.18	0.22	0.13
SDI	0.79	-0.33	0.30	0.43	0.44	0.94	0.99	0.44	0.44	0.11	0.68	0.47	0.80
RDI	0.79	-0.33	0.30	0.43	0.44	0.94	0.99	0.44	0.44	0.11	0.68	0.47	0.80
DI	0.90	-0.05	0.56	0.66	0.66	0.85	0.91	0.68	0.68	0.39	0.87	0.70	0.94
SSPI	0.74	-0.41	0.23	0.36	0.37	0.94	1.00	0.38	0.38	0.04	0.62	0.40	0.75
GM	-0.05	0.16	0.08	0.11	0.13	-0.15	-0.14	0.09	0.09	0.12	-0.01	0.11	-0.07
ATI	0.69	-0.48	0.15	0.29	0.30	0.93	0.99	0.30	0.30	-0.05	0.56	0.33	0.70
SNPI	0.01	0.35	0.25	0.24	0.27	-0.22	-0.21	0.23	0.23	0.30	0.09	0.24	0.01
RDY	0.86	0.60	0.97	0.99	1.00	0.40	0.37	0.97	0.97	0.90	0.91	0.96	0.84
DTE	0.79	-0.33	0.30	0.43	0.44	0.94	0.99	0.44	0.44	0.11	0.68	0.47	0.80
b	0.50	-0.41	0.06	0.19	0.20	0.71	0.65	0.11	0.11	-0.09	0.28	0.12	0.39
bN	-0.24	0.11	-0.07	-0.13	-0.11	-0.29	-0.30	-0.09	-0.09	-0.02	-0.16	-0.09	-0.21
DRI	0.94	0.22	0.76	0.83	0.83	0.70	0.76	0.86	0.86	0.63	0.97	0.87	0.99

	Pi	SDI	RDI	DI	SSPI	GM	ATI	SNPI	RDY	DTE	b	S^2	bN	DRI
Pi	1													
SDI	-0.05	1												
RDI	-0.05	1.00	1											
DI	0.03	0.94	0.94	1										
SSPI	-0.06	0.99	0.99	0.91	1									
GM	0.17	-0.13	-0.13	-0.17	-0.13	1								
ATI	-0.08	0.97	0.97	0.86	0.99	-0.15	1							
SNPI	0.20	-0.17	-0.17	-0.14	-0.21	0.95	-0.25	1						
RDY	0.24	0.44	0.44	0.66	0.37	0.13	0.30	0.26	1					
DTE	-0.05	1.00	1.00	0.94	0.99	-0.13	0.97	-0.17	0.44	1				
b	-0.11	0.64	0.64	0.55	0.65	-0.12	0.64	-0.15	0.20	0.64	1			
bN	-0.02	-0.31	-0.31	-0.26	-0.30	0.01	-0.31	0.02	-0.11	-0.31	-0.53	0.26	1	
DRI	0.12	0.81	0.81	0.95	0.76	-0.07	0.71	0.00	0.83	0.81	0.39	0.33	-0.22	1

characterized by drought tolerance criteria and will improve yield under stress conditions.

These observed relationships are in consistence with numerous studies. Many studies reported positive relationships between Ys and the most popular and widely used indices MP, GMP, STI, SSI, TOL (Khalili et al., 2004; Golabadi et al., 2006; Gholinezadeh et al., 2010, Mohammadi et al., 2010, Farshadfar et al., 2012a, Mevlut et Sait, 2011; Nouri et al., 2011; Mevlut and Sait, 2011; İlker et al., 2011; Reza Eivazi et al., 2013; Rahmani et al., 2013**)**. Jafari et al. (2009); Gholinezadeh et al. (2010), Farshadfar and Elyasi (2012) and Farshadfar et al. (2012b, 2013, 2014) noticed also positive significant correlation between YS and HM, YI, DI, MSTIk1, MSTIk2 and DRI. The coefficient of regression (b) expressed significant positive correlation with yield under stress to

Table 6. Spearman's rank correlation coefficients between yields and drought tolerance indices 2015.

	YS	YP	MP	MRP	REI	SSI	TOL	GMP	STI	MSTIk1	MSTIk2	HM	YI
YS	1												
YP	0.31	1											
MP	0.86	0.71	1										
MRP	0.93	0.59	0.98	1									
REI	0.93	0.58	0.98	0.99	1								
SSI	0.91	-0.07	0.62	0.74	0.74	1							
TOL	0.80	-0.27	0.44	0.57	0.58	0.97	1						
GMP	0.93	0.58	0.98	0.99	1.00	0.74	0.58	1					
STI	0.93	0.58	0.98	0.99	1.00	0.74	0.58	1.00	1				
MSTIk1	0.72	0.85	0.96	0.91	0.91	0.42	0.23	0.91	0.91	1			
MSTIk2	0.99	0.40	0.91	0.97	0.97	0.87	0.74	0.97	0.97	0.79	1		
HM	0.96	0.49	0.95	0.99	0.99	0.81	0.67	0.99	0.99	0.85	0.99	1	
YI	1.00	0.31	0.86	0.93	0.93	0.91	0.80	0.93	0.93	0.72	0.99	0.96	1
Pi	-0.04	0.10	0.03	0.04	0.03	-0.12	-0.17	0.03	0.03	0.09	-0.04	-0.02	-0.04
SDI	0.91	-0.07	0.62	0.74	0.74	1.00	0.97	0.74	0.74	0.42	0.87	0.81	0.91
RDI	0.91	-0.07	0.62	0.74	0.74	1.00	0.97	0.74	0.74	0.42	0.87	0.81	0.91
DI	0.97	0.12	0.75	0.85	0.85	0.97	0.90	0.85	0.85	0.57	0.94	0.90	0.98
SSPI	0.80	-0.27	0.44	0.57	0.58	0.97	1.00	0.58	0.58	0.23	0.74	0.67	0.80
GM	0.80	0.08	0.66	0.72	0.75	0.85	0.82	0.75	0.75	0.53	0.79	0.80	0.80
ATI	0.56	-0.55	0.13	0.27	0.28	0.83	0.93	0.28	0.28	-0.09	0.47	0.39	0.56
SNPI	0.87	0.31	0.81	0.85	0.87	0.81	0.73	0.87	0.87	0.71	0.88	0.90	0.87
RDY	0.93	0.58	0.98	0.99	1.00	0.74	0.58	1.00	1.00	0.91	0.97	0.99	0.93
DTE	0.91	-0.07	0.62	0.74	0.74	1.00	0.97	0.74	0.74	0.42	0.87	0.81	0.91
b	0.79	-0.26	0.43	0.56	0.57	0.96	0.99	0.57	0.57	0.22	0.72	0.65	0.79
bN	0.91	-0.05	0.63	0.74	0.74	0.99	0.96	0.74	0.74	0.43	0.86	0.80	0.91
DRI	0.95	0.04	0.69	0.79	0.80	0.97	0.92	0.80	0.80	0.50	0.91	0.86	0.95

	Pi	SDI	RDI	DI	SSPI	GM	ATI	SNPI	RDY	DTE	b	S^2	bN	DRI
Pi	1													
SDI	-0.12	1												
RDI	-0.12	1.00	1											
DI	-0.09	0.97	0.97	1										
SSPI	-0.17	0.97	0.97	0.90	1									
GM	-0.17	0.85	0.85	0.83	0.82	1								
ATI	-0.21	0.83	0.83	0.71	0.93	0.69	1							
SNPI	-0.12	0.81	0.81	0.85	0.73	0.96	0.52	1						
RDY	0.03	0.74	0.74	0.85	0.58	0.75	0.28	0.87	1					
DTE	-0.12	1.00	1.00	0.97	0.97	0.85	0.83	0.81	0.74	1				
b	-0.22	0.96	0.96	0.89	0.99	0.81	0.93	0.72	0.57	0.96	1			
bN	-0.17	0.99	0.99	0.96	0.96	0.84	0.82	0.81	0.74	0.99	0.96	0.18	1	
DRI	-0.15	0.97	0.97	0.98	0.92	0.83	0.75	0.82	0.80	0.97	0.90	0.11	0.96	1

Bold values are significant at 5% level of probability.

identify the drought tolerant genotypes in Guttieri et al. (2001), Clarke et al. (1992), Ahmadi et al. (2004), Moghaddam and Hadizadeh (2002), Mevlut and Sait (2011) and Khadarahmpour et al. (2011). Gholinezadeh et al. (2010) and Mohammadi et al. (2012) reported also significant positive correlation between RDI and Ys. Significant relationships between YS and REI, MRP and between Ys and DTE were also reported by Singh et al. (2011) and Kumar et al. (2014). Naghavi et al. (2013) observed significant differences between Ys and SSPI. This finding was in agreement with Naghavi et al. (2013) and in contradiction with Farshadfar et al. (2012a, 2014;

Moosavi et al., 2008).

The correlation between YS and SNPI disappeared when the stress reached 43% of intensity. However, many studies confirmed this significant positive correlation (Farshadfar et al., 2012a; 2012b; 2014; Moosavi et al., 2008). The same pattern was observed bewteen Ys and GM. Mohammadi et al. (2011, 2012) found a significant positive correlation between YS and GM at 22.6 and 26.4% stress intensity. On the other hand, the relationships between YS and SDI, RDY disagreed with the findings of Farshadfar et al. (2012b). The positive correlation between Ys and ATI was in disagreement with the results of Farshadfar et al. (2012a, 2012b); Moosavi et al. (2008) which attested the absence of relationship between those two indices.

Under non-stressed environment, yield (Yp) during 2014 season (43% of stress intensity) was highly and positively correlated with MP, MRP, GMP, STI, MSTIk1, HM, RDY and REI; moderately correlated with MSTIk2 (0.39) (Table 5). During 2015 (32% of stress intensity), the same correlations were obtained with more moderate association (<0.4), except for MSTIk2 and RDY (which remained almost the same) and ATI (stronger correlation with YF) (Table 6). Moreover, the moderate positive correlation with TOL, SNPI and the negative ones with SSI, SDI, RDI, SSPI, DTE and b were lost (Table 6). Based on the two cropping season results, the yield under favorable conditions (Yp) had strong positive repeatable correlation with MP, MRP, REI, GMP, STI, MSTIk1, HM, RDY; moderate correlation with MSTIk2 and significant negative correlation with ATI. Those indices permit to select genotypes with high yield potential (Yp). They are also influenced by the variation between yield under stressed and non-stressed conditions except RDY and MSTIk2.

The positive correlations observed between Yp and (MSTIk1, MP, GMP, STI, MSTIk2, HM and RDY) are in agreement with the results obtained by Moosavi et al. (2008), Gholinezhad et al. (2014); Farshadfar et al. (2012b;, 2013); Mevlut and Sait (2011), Farshadfar and Elyasi (2012) and Naghavi et al. (2013). However, the absence or the negative correlation between Yp and SSI, TOL, SSPI, SNPI, YI and DI are in disagreement with the same authors. Non-significant correlations between SSI and Yp were found in Ahmadi et al. (2004), Golabadi et al. (2006), Moosavi et al. (2008), Khodarahmpour et al. (2011), Drikvand et al. (2012), Mohammadi et al. (2012), Farshadfar et al. (2014) and Mohammadi et al. (2011). The presence of negative correlation between TOL and Yp under moderately severe conditions (60%) in comparison with moderate conditions (34%) was also found by Mohammadi et al. (2011) and the absence of correlation was reported in other studies (Moosavi et al., 2008; Khodarahmpour et al., 2011). Moosavi et al. (2008), Farshadfar et al. (2012b) and Naghavi et al. (2013) obtained positive correlation between Yp, SSPI and SNPI. However, the absence of correlation between SSPI and Yp found in our study was in agreement with Farshadfar and Elyasi (2012). Moreover, the non-significant correlation between Yp and DI was in agreement with the results obtained by Farshadfar et al. (2012b). Similar to our findings, REI and MRP were useful in identifying genotypes with high yield potential in Singh et al. (2011). Furthermore, no correlation were found between (Pi, b, bN, YSI) and Yp as supported by Mohammadi et al. (2011).

In this study, no significant associations were found between Pi and the yield under both conditions. The same finding was observed in Mevlut and Sait (2011), however, this is not in agreement with other studies (Mohammadi et al., 2010; Mevlut and Sait, 2011). Moreover, our findings were in disagreement with the results obtained by Mohammadi et al. (2012) concerning the correlation between Yp and GM, RDI, YSI and DRI. In addition, the negative correlation between ATI and Yp is in disagreement with Moosavi et al. (2008) and Farshadfar et al. (2012, 2012a); Rahmani et al. (2013) where there was a positive association.

Overall, under moderate stress, the drought indices MP, MRP, REI, GMP, STI, MSTIk1, MSTIk2, HM and RDY were correlated with both moisture conditions (non-stressed and stressed) during the two cropping seasons. Thus, they can be considered as repeatable suitable criteria for selection for drought tolerant and high yielding genotypes. These results can be supported by numerous studies (Golabadi et al., 2006; Boussen et al., 2010; Nouraein et al., 2013; Farshadfar and Sutka, 2002; Ilker et al., 2011; Jafari et al., 2009; Mohammadi et al., 2003; 2010; 2011; Khodarahmpour et al., 2011; Farshadfar and Elyasi, 2012; Farshadfar et al., 2012a, b; 2013; Drikvand et al., 2012; Naghavi et al., 2013).

Relationships between drought tolerance indices

The relationships between the different drought indices will allow us to suggest one as alternative for the others that belong to the same group based on their strong correlation for the evaluation of the drought tolerant and high yielding genotypes. In the presence of a large number of indices, the principal component analysis (PCA) was used to assess in a simple graphic the relationships, similarities and dissimilarities between all attributes at once, based on the rank correlation.

In 2014 cropping season, the first and second components explained 80% of the total variation (55.5 and 24.2% respectively) (Figure 2). The PCA1 and PCA2 mainly distinguish the indices in different groups. The yield under stress (YS) and the indices MP, MRP, REI, SSI, TOL, GMP, STI, MSTIk2, HM, YI, SDI, RDI, DI, SSPI, ATI, RDY, DTE and DRI were correlated with the first component. This component can be called “stress tolerance component”. The cosine of the angle between the vectors of two indices approximates the correlation

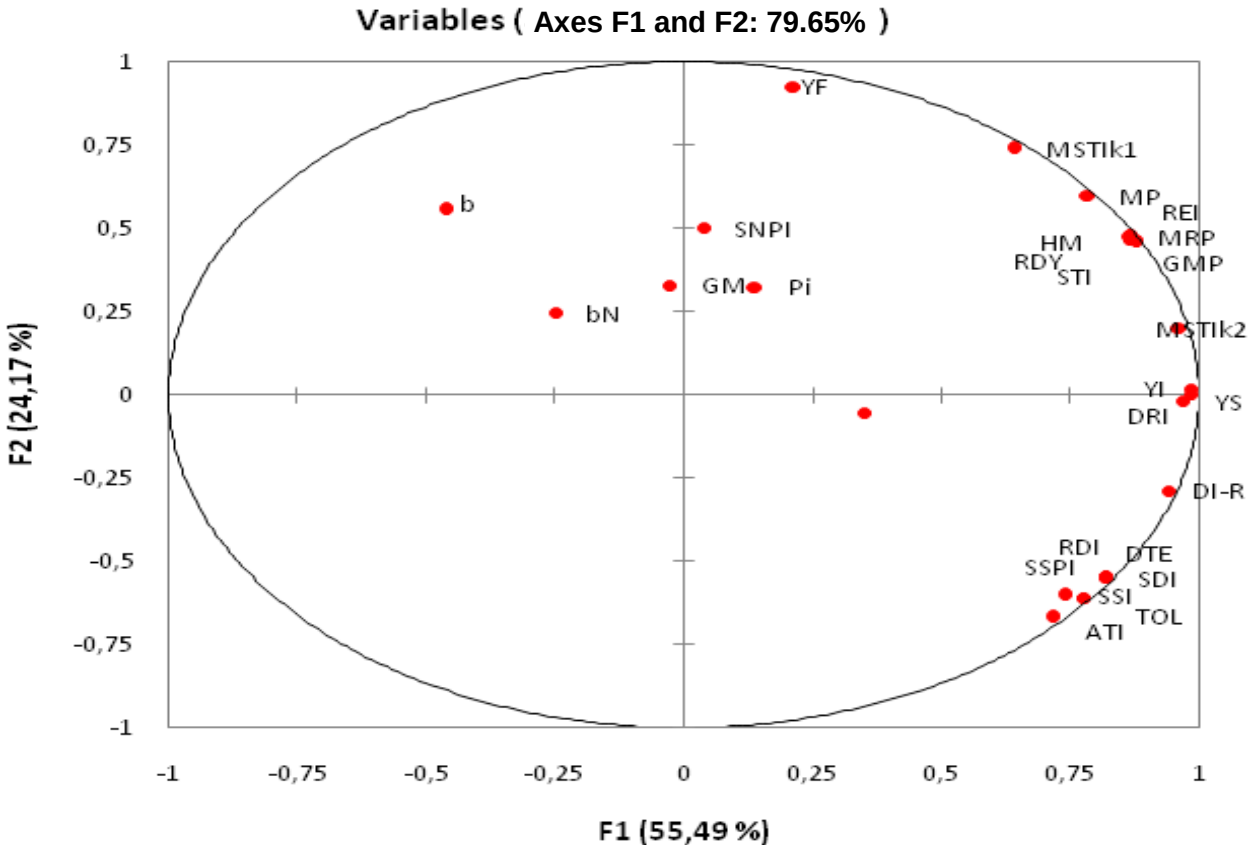

Figure 2. Biplot of drought indices based on principal component analysis for 2013-14 season.

between them. The angle between MSTIk1, MSTIk2, MP, MRP, RDY, HM, STI, GMP, REI, DRI, YI and DI was well below 90° (acute angle) showing high correlations and similarities in ranking the genotypes (0.64 <coefficient of correlation (r) < 0.99); except for DI which showed moderate correlations. Inside this group, an overlapping of vectors (zero angle) was found between RDY, HM, STI, GMP, MRP, and REI (0.96< r < 1) and between YI and DRI (r = 0.999) showing same ranking genotypes basis. Similar relationships were observed between SSI, ATI, DTE, TOL, SDI, SSPI and RDI (0.93< r <1) indicating that these indices are identical in genotype rankings. The second component PCA2 was highly positively correlated with the potential yield (Yp) and MSTIk1 (r = 0.87) and moderately correlated to the coefficient of regression (b) (r = 0.41). This component can be called “yield potential component”. The index MSTIk1 had positive and strong correlation to both components but with more emphasis on the stress tolerance component. The indices GM and SNPI were correlated to PCA3 whereas bN was correlated to PCA4; those two components explained only 6.5 and 5% respectively of variation between the indices. Finally, Pi was correlated to PCA5 which explained 3.45% of variation. Thus, the indices (GM, SNPI, bN and Pi) had low contribution to the variation between genotypes.

In 2015 cropping season, the first and second components explained 90.3% of the variation between all indices in 2015 (Figure 3). YS, MP, MRP, REI, SSI, TOL, GMP, STI, MSTIk2, HM, YI, SDI, RDI, DI, SSPI, GM, SNPI, RDY, DTE, DRI, bN were positively correlated with PCA1 (73% of variation), whilst b had negative correlation. The angle between MSTIk1, MSTIk2, MP, MRP, RDY, STI, GMP, REI, HM, YI and SNPI was well below 90 degrees showing similarities in ranking the genotypes (0.83<r<1). An acute angle was observed between MRP, GMP, RDY, STI and REI (0.997<r< 1) displaying that these indices are identical in genotype rankings. An acute angle was also found between YS, SNPI and YI (0.87<r<1). Similar relationships were observed between TOL, SSPI, bN, DTE, RDI, SDI, SSI, GM, DI and DRI with an angle below 90° (0.81<r<1). A zero angle was found between SSI, SDI, bN, DTE and RDI (0.99<r<1). A zero angle was found between TOL and SSPI (r = 1), indicating that they ranked similarly the genotypes, as indicated by the zero angle between their vectors. Similar relationships were observed GM, DI and DRI (0.82<r<0.98). The PCA2 (17% of variation) is correlated positively with Yp, MSTIk1 and negatively with ATI. The grain yield (Yp) was highly correlated to MSTIK1 (r = 0.85) and moderately negatively correlated to ATI (r = -0.55). Similarly to the first year, the index MSTIk1 had

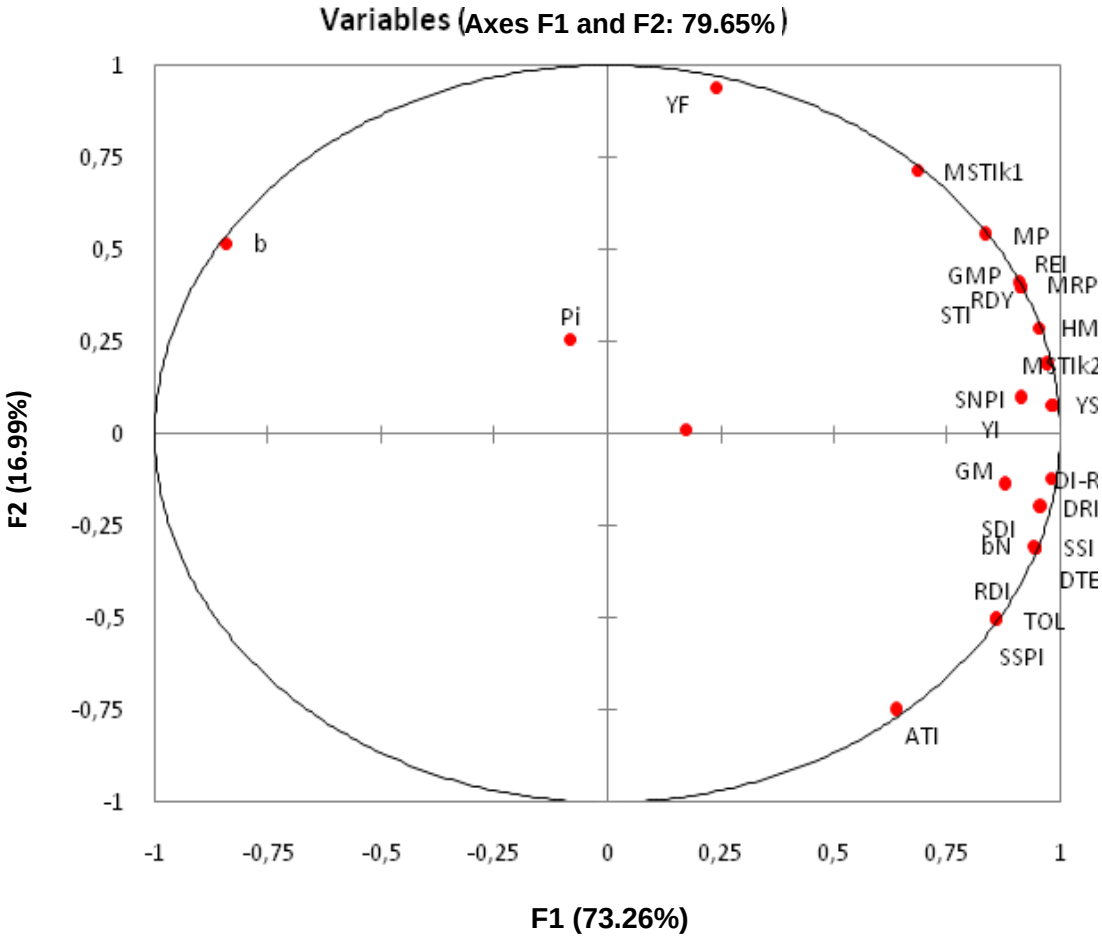

Figure 3. Biplot of drought indices based on principal component analysis for 2014-15 season.

positive and strong correlation to both components but with more emphasis on the first one. Finally, Pi had significant moderate correlation with PCA3 which explained only 4% of total variability.

Based on the results obtained in two cropping seasons, no relationship was found between the grain yield in non-stressed and stressed environments as indicated by their correlation to different components and by the right angle between their vectors. Strong repeatable significant correlations were found between MRP, RDY, STI, GMP, REI, HM, MP, YI, MSTIk1 and MSTIk2. This indicated that one of these indices could be used interchangeably as an alternative for the others in genotypes selection, especially the first 5 ones. The observed relationships are in concordance with those observed by Normand et al. (2001), Golabadi et al. (2006), Mevlut and Sait (2011), Mohammed et al. (2011, 2012), Drikvand et al. (2012), Moradi et al. (2012), Farshadfar et al. (2012a, b), Reza Eivazi et al. (2013), Rahmani et al. (2013), Naghavi et al. (2013) and Farshadfar et al. (2014). Strong repeatable relationships were also observed between SSI, TOL, SDI, RDI, DTE and SSPI. Similar findings were reported by Normand et al. (2001), Golabadi et al. (2006), Boussen et al. (2010), Mohammadi et al. (2010, 2012), Dadbakhsh et al. (2011), Farshadfar et al. (2012a, b), Rahmani et al. (2013) and Farshadfar et al. (2014). No correlation was found between the superiority index (Pi) and the other drought indices. Those findings were not in agreement with the findings of Mohammadi et al. (2010) and Melvut and Sait (2011).

Screening genotypes

Tables 7 and 8 represent the average mean yield, variance between genotypes and mean variance of the top 20% genotypes selection based on each index ranking during the two cropping seasons. Those parameters will be able to define the drought indices provinding the best accurate genotypes selection at 20% selection pressure.

During the first cropping season 2014 (Table 7), mean values of indices showed similarities in top ranking genotypes for MP, MRP, REI, GMP, MSTIk1, HM, RDY and STI. The top similar genotypes for this group were 2, 6, 9, 10 and 11. The indices DI, SSI, TOL, SDI, RDI,

Table 7. Descriptive statistics of the top 20% genotype selection for drought indices during 2013-2014.

Indices	Mean yield of 20% top genotypes	Variance inter 20% genotypes	Mean variance of the top genotypes	Top 20% genotypes selected
ATI	2.70	0.13	0.53	30, 2, 21, 8, 37, 11, 39, 36
b	2.68	0.12	0.38	24, 40, 5, 26, 35, 18, 17, 23
bN	2.78	0.07	0.14	7, 3, 9, 25, 15, 14, 31, 6
DI	2.77	0.11	0.14	2, 30, 21, 8, 11, 23, 36, 37
DRI	2.99	0.03	0.46	2, 11, 21, 8, 23, 9, 1, 17
DTE	2.70	0.13	0.53	30, 21, 37, 8, 2, 39, 11, 36
GM	2.70	0.12	0.60	1, 20, 4, 32, 9, 31, 12, 27
GMP	3.08	0.02	0.14	2, 9, 11, 6, 17, 10, 23, 4
HM	3.08	0.02	0.59	2, 9, 11, 6, 17, 10, 23, 4
MP	3.10	0.01	0.28	2, 6, 9, 10, 11, 17, 19, 31
MRP	3.10	0.01	0.63	2, 11, 9, 6, 10, 34, 4, 31
MSTIk1	3.10	0.01	0.95	6, 2, 9, 10, 17, 11, 19, 31
MSTIk2	3.03	0.03	0.59	2, 11, 9, 23, 8, 21, 17, 6
Pi	2.73	0.09	0.14	18, 31, 22, 11, 26, 9, 15, 3
RDI	2.70	0.13	0.14	30, 21, 37, 8, 2, 39, 11, 36
RDY	3.10	0.015	0.53	2, 9, 11, 6, 10, 34, 4, 31
REI	3.10	0.015	0.53	2, 9, 11, 6, 10, 34, 4, 31
SDI	2.70	0.13	0.42	30, 21, 37, 8, 2, 39, 11, 36
SNPI	2.94	0.02	0.81	1, 20, 4, 9, 31, 17, 19, 34
SSI	2.70	0.13	0.14	30, 21, 37, 39, 8, 2, 11, 36
SSPI	2.70	0.13	0.34	30, 21, 8, 2, 37, 39, 11, 36
STI	3.08	0.02	0.14	2, 9, 11, 6, 17, 10, 23, 4
TOL	2.70	0.13	0.16	30, 21, 8, 2, 37, 39, 11, 36
YI	2.99	0.03	0.63	2, 11, 8, 21, 23, 9, 1, 17

SSPI, ATI and DTE selected the genotypes 30, 21, 37, 39, 8, 2 and 11 as best performances. The genotypes 2, 11, 9, 23, 8, 21 and 17 were the best selections for MSTIk2 and YI. According to GM and SNPI, the genotypes 1, 20, 4, 32, 9 and 31 exhibited the best rankings. The superiority index (Pi) selected the genotypes 18, 31, 22, 11 and 26. The coefficient of regression (b) identified the genotypes 24, 40, 5, 26 and 35 as best performances. The least values of the index bN were obtained by the genotypes 7, 3, 9, 25, 14 and 15. Finally, the highest values of DRI were obtained by the genotypes 2, 11, 21, 8, 23 and 9.

During the second season 2015 (Table 8), the indices MP, MRP, REI, GMP, STI, MSTIk1, MSTIk2, HM, YI and RDY selected the genotypes 11, 8, 9, 34, 10, 28 and 6 as top ranking. Similarly, SSI, TOL, SDI, RDI, DI, SSPI, DTE, bN, DRI, GM and SNPI selected the genotypes 2, 14, 9, 8 and 10 as best performances; except for the genotype 2 which was not selected by GM and SNPI. The least values of Pi were exhibited by the genotypes 16, 22, 33, 31, 15 and 18. The genotypes 5, 21, 16, 18, 29 and 37 expressed the lowest values of b. Finally, the genotypes 2, 14, 38, 9, 1, 20 and 40 were the top rankings for the index ATI.

Based on those results, the similarities between drought indices in genotypes selection were in concordance with the previous correlation and biplot results. These findings showed that the indices MP, MRP, REI, GMP, MSTIk1 and HM ranked similarly the genotypes. Their values are based on relative performance under various moisture conditions with little emphasis on yield stability. They have higher power in the separation of group A from the other Fernandez groups (Rosielle and Hamblin, 1981; Fernandez, 1992; Ramirez and Kelly, 1998; Golabadi et al., 2006; Talebi et al., 2009; Singh et al., 2011). The drought index RDY belonged also to the same grouping in the present study; even if this index emphasize on the selection of genotypes which have the minimum reduction in grain yield due to the moisture stress (Deshmukh et al., 2004); so it is more related to yield stability. For MSTIk2 and YI, they were affiliated to this grouping only during 2015 when the stress intensity was 32%. Once the stress became harder during 2015 (43% of yield reduction), they constituted a separate common group because their formulation (equation) is based mainly on yield under stress conditions (Gavuzzi et al., 1997; Singh et al., 2011; Rahmani et al., 2013) in comparison to the other indices. In contrast, DI, SSI, TOL, SDI, RDI, DI, SSPI, DTE, bN and DRI emphasized more on yield stability and low

Table 8. Descriptive statistics of the top 20% genotype selection for drought indices during 2014-2015 cropping season.

Indices	Mean yield of 20% top genotypes	Variance inter 20% genotypes	Mean variance top 20% genotypes	Top 20% Genotypes selected
ATI	3.80	0.26	0.13	2, 14, 38, 9, 1, 20, 40, 8
b	3.96	0.23	0.12	5, 21, 16, 18, 29, 37, 23, 26
bN	4.14	0.16	0.13	2, 14, 9, 8, 10, 34, 1, 32
DI	4.29	0.20	0.14	2, 8, 9, 14, 11, 10, 34, 32
DRI	4.31	0.20	0.16	2, 8, 14, 9, 11, 6, 10, 34
DTE	4.14	0.16	0.13	2, 14, 9, 8, 10, 34, 1, 32
GM	4.16	0.14	0.15	14, 9, 8, 10, 34, 1, 32, 20
GMP	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6, 32
HM	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6, 32
MP	4.46	0.06	0.30	11, 8, 9, 34, 10, 28, 6
MRP	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6
MSTIk1	4.46	0.06	0.33	11, 8, 9, 34, 10, 28, 6, 3
MSTIk2	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6, 32
Pi	3.56	0.25	0.85	16, 22, 33, 31, 15, 18, 9, 27
RDI	4.14	0.16	0.13	2, 14, 9, 8, 10, 34, 1, 32
RDY	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6, 32
REI	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6
SDI	4.14	0.16	0.13	2, 14, 9, 8, 10, 34, 1, 32
SNPI	4.38	0.13	0.19	14, 8, 9, 11, 10, 34, 32, 28
SSI	4.14	0.16	0.13	2, 14, 9, 8, 10, 34, 1, 32
SSPI	3.96	0.23	0.12	2, 14, 9, 8, 1, 20, 38, 10
STI	4.46	0.06	0.26	11, 8, 9, 34, 10, 28, 6, 32
TOL	3.96	0.23	0.12	2, 14, 9, 8, 1, 20, 38, 10
YI	4.40	0.14	0.22	11, 8, 9, 10, 34, 2, 28, 6

changes between potential and actual yields under moisture conditions. In this case, top ranking genotypes are not necessarily high yielding (Fischer and Maurer, 1978; Fernandez, 1992; Clarke et al., 1992; Ramirez and Kelly, 1998; Guttieri et al., 2001; Sio- Se Mardeh et al., 2006; Golabadi et al., 2006). GM and SNPI had the same top ranking genotypes as SSI, TOL, SDI, RDI, DI, SSPI, DTE, bN and DRI during 2015. However, when the gap between the potential yield and yield under stress became larger (43% of reduction during 2014), those two indices were grouped together in a separate cluster because they put more emphasis on yield stability and high yield under stressed conditions (Farshadfar et al., 2002; Moradi et al., 2012) compared to the other indices.

The best indices should be able to select the highest and stable performances. Based on the mean yield and mean variance of the 20% top genotypes selection (Tables 7 and 8), the indices MP, MRP, REI, RDY, GMP, STI, HM, MSTIk1 and MSTIk2 identified the highest mean yields during 2014 (3.09 t/ha) and 2015 (4.47 t/ha) cropping seasons. In contrast, the mean variance of the top 20% genotypes varied from 0.14 to 0.95 in 2014 and from 0.26 to 0.33 during 2015. Thus, the mean variance between yield under stress and non-stress environments became higher at 43% of drought intensity compared to 32%. However, the indices GMP, MP and STI were able to exhibit the best combination of high mean yield and low mean variance.

Conclusion

The indices MP, MRP, REI, GMP, STI, MSTIk1, MSTIk2, HM and RDY showed high discrimination between genotypes, exhibited the best correlation with both yields under stressed and non-stressed environments and were able to identify the highest mean yielding genotypes with low variance across environments, especially STI, GMP and MP. These indices can be considered as suitable criteria for selection of drought tolerant and high yielding genotypes under moderate stress Mediterranean environment. The indices MP, MRP, REI, GMP, STI and RDY can be used interchangeably. The genotypes “AUS30355” and “Gladius” were recognized as best stable performances in the different moisture conditions. Our conclusions may be limited in terms of drought scenarios (duration, timing). The stress severity of our stressed environments was moderate consisting of drought at mid-stage (pre-flowering and flowering). More stress severities and drought scenarios may need to be

studied before confirming the general suitability of the different indices. Practically, these indices can be used immediately for semi arid environments of moderate drought severity, like areas located north of the latitude 33°N. Moreover, one particular disadvantage of these indices is their limitation on two contrasting environments at a time only, while the breeding for large adaptation usually uses a network of a wide range of environments. A development of data processing software will be useful in this case.

Abbreviations: ATI, abiotic tolerance index; **GM,** golden mean; **GMP,** geometric mean productivity; **HM,** harmony mean; **MP,** mean productivity; **MRP,** mean relative performance; **MSTIk1,** modified stress tolerance index 1; **MSTIk2,** modified stress tolerance index 2; **RDY,** relative decrease in yield; **REI,** relative efficiency index; **STI,** stress tolerance index; **SNPI,** stress/non-stress production index.

Conflict of Interests

The authors have not declared any conflict of interests.

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